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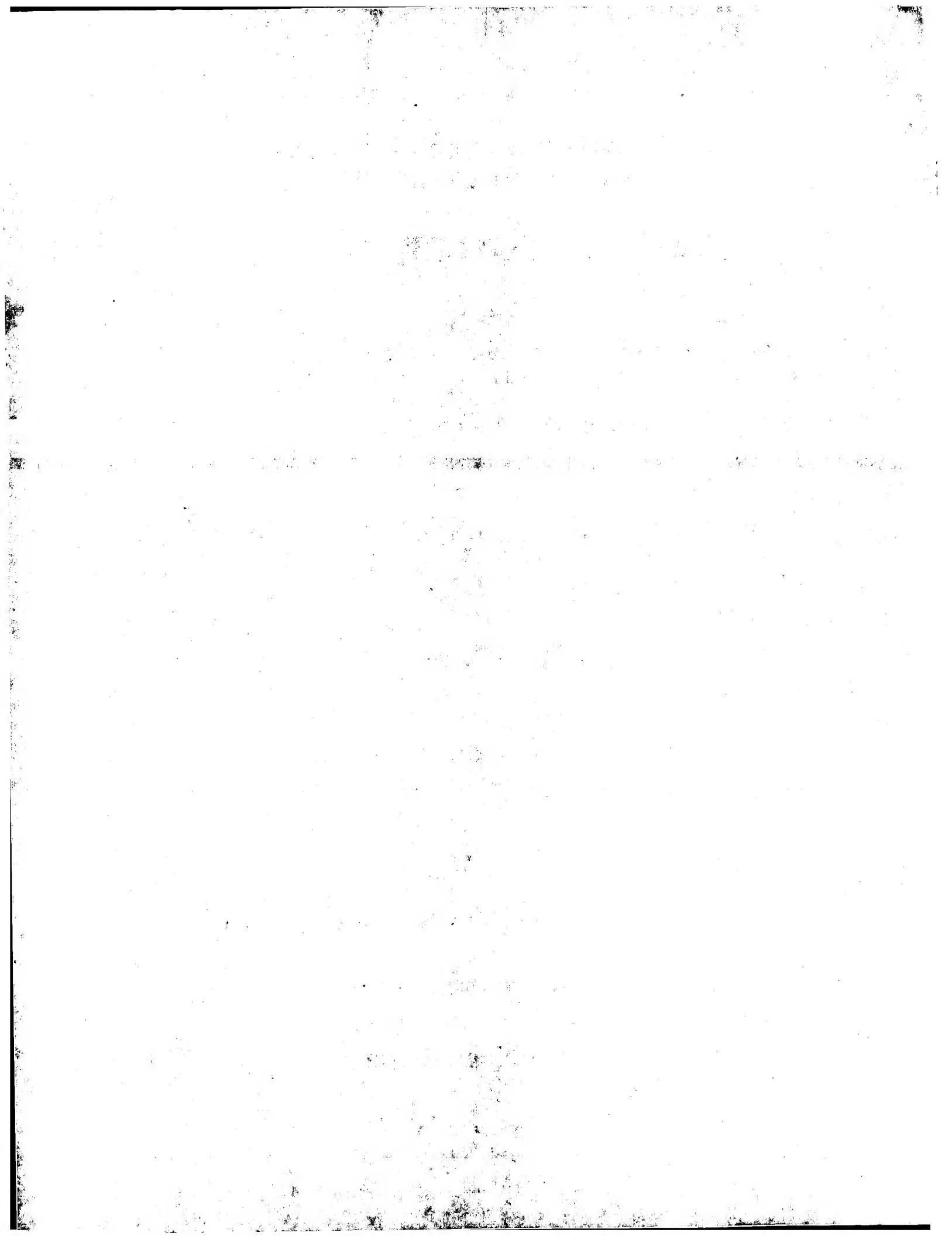
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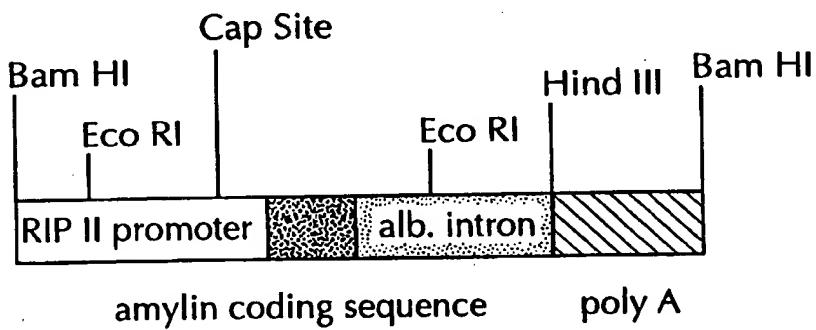
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(54) Title: TRANSGENIC ANIMAL MODELS FOR TYPE II DIABETES MELLITUS



(57) Abstract

The generation of transgenic animal models for testing various treatments of Type II Diabetes Mellitus are described. The DNA construct allows pancreatic β cell - specific expression of human islet associated polypeptide (IAPP) under the regulation of the rat insulin II promoter in both cell lines and transgenic animals. The DNA construct is introduced into animal embryos by microinjection as one or multiple copies or into established cell lines by electroporation. The transgenic animals develop amyloid plaque deposits in the islets of Langerhans in the pancreas, fasting hyperglycemia, glycuria and diabetic glomerulosclerosis at 3 to 5 months of age. The cell lines can be screened for treatments that inhibit expression of human IAPP; the transgenic animals can be screened for treatments that either enhance or inhibit the progression of this disease phenotype.

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TRANSGENIC ANIMAL MODELS FOR TYPE II DIABETES MELLITUSBackground of the Invention

This invention relates to a process for genetic alteration of mammalian cell lines and animals such that they express the protein encoded by the human Islet Amyloid Polypeptide (IAPP) gene. IAPP, formerly known as amylin, is the major protein 10 component of pancreatic islet amyloid that forms in the pancreata of Non-Insulin Dependent Diabetes Mellitus (NIDDM) patients. Recent studies of IAPP structural and functional characteristics suggest that IAPP, along with insulin and other hormones, plays a major role in carbohydrate metabolism. IAPP is produced, stored and secreted by pancreatic β cells in the islets of Langerhans. It can mimic the phenomenon of 15 insulin resistance seen in NIDDM by inhibiting glucose uptake and glycogen synthesis in muscle, and liver tissue. The generation of amyloid deposits in humans is thought to be due to the ability of the center portion of the peptide (amino acids 20-29) to form a β pleated sheet structure. Rodent IAPP differs from human IAPP in that the 20 sequences in this otherwise highly conserved protein between amino acids 20-29 are not conserved and amyloid deposits do not form in rodent pancreata. A working hypothesis is that overexpression of human IAPP leads to insulin resistance in peripheral tissues and in the formation of amyloid deposits.

Transgenic animals, especially mice, have proven to be very useful in dissecting complex systems to generate new information about human disease. Selective 25 expression of human genes in such mice has generated novel model systems to study disease, especially when overexpression of a gene results in a disease state. With such transgenic mice, one can address issues concerning (1) tissue specificity of expression; (2) testing of hypotheses that overexpression of a particular gene leads to disease; (3) the number and identity of tissues/organs that are affected by this 30 overexpression; and (4) effects of various treatments, including drugs, on the progression or amelioration of the disease phenotype.

The generation of transgenic mice that express human IAPP has been reported in the literature, though none of these animals developed a diabetic phenotype. Niles Fox et al. (FEBS Letters 323, 40-44 [1993]) constructed a transgene that fused the rat 35 insulin promoter sequence to a genomic DNA fragment containing the entire human IAPP gene (exons 1-3 and introns 1 and 2). Transgene RNA expression was detected in pancreas, anterior pituitary and brain. Although plasma IAPP levels were 5-fold

elevated relative to nontransgenic littermates, no metabolic consequence of this elevation was observed. C.B. Verchere et al. (Diabetologia 37, 725-729 [1994]) used a 600 bp fragment encoding the entire human proIAPP sequence. Their transgenic animals exhibited greater pancreatic content of both IAPP and insulin relative to 5 nontransgenic littermate controls. Increased secretion of both hormones was also detected in perfused pancreas studies. No clinical manifestations of this enhanced storage and secretion were observed. Höppener et. al. (Diabetologia 36, 1258-1265 [1993]) described the generation of multiple transgenic lines that expressed either human or rat IAPP in the mouse endocrine pancreas. Höppener's group used a 703 10 bp rat insulin II promoter fragment to drive expression of human or rat IAPP from genomic DNA fragments. Plasma IAPP levels were up to 15 fold elevated but no hyperglycemia nor hyperinsulinemia were observed. In a subsequent study, no amyloid plaque was seen to accumulate in vivo but intra- and extracellular amyloid fibrils did form when islets from these transgenics were cultured in vitro under conditions 15 mimicking hyperglycemia (De Koning et al. Proc. Natl. Acad. Sci. 91, 8467-8471 [1994]).

Summary of the Invention

In one embodiment, the present invention is directed to recombinant DNA comprising a non-IAPP promoter, a sequence encoding human IAPP or an active fragment thereof functionally linked to a human albumin intron I encoding sequence, 20 a human GAPDH termination encoding sequence and a human GAPDH polyadenylation encoding sequence, said DNA resulting in expression of a diabetic phenotype when incorporated into a suitable host.

Especially preferred is recombinant DNA wherein the non-IAPP promoter is selected from the group consisting of promoters for the genes for rat insulin I, rat 25 insulin II, human insulin, mouse IAPP, rat beta cell-specific glucokinase, glucose transporter 2, human tyrosine amino transferase, human albumin, mouse albumin, rat liver specific glucokinase, and mouse metallothionein.

Also preferred is recombinant DNA wherein said promoter is the rat insulin II promoter.

30 Especially also preferred is recombinant DNA wherein said sequence encoding human IAPP or an active fragment thereof has the characteristics of cDNA.

Further preferred is recombinant DNA wherein said sequence encoding human IAPP or an active fragment thereof has the characteristics of genomic DNA.

Also further preferred is recombinant DNA wherein said sequence is that of SEQ ID NO: 4.

Also especially further preferred is recombinant DNA wherein said sequence of cDNA is that of SEQ ID NO: 5.

5 In another embodiment, the DNA sequence encoding human IAPP is replaced by a DNA sequence encoding mouse IAPP or an active fragment thereof, with said mouse DNA preferably having the characteristics of cDNA.

The present invention is also directed to vectors comprising recombinant DNA of the present invention (SEQ. ID NO: 1).

10 The present invention is also directed to an eukaryotic cell line comprising recombinant DNA of the present invention with preferred cell lines selected from the group consisting of rat insulinoma (RIN) cells, hamster insulinoma (HIT) cells and β -TC3 mouse insulinoma cells.

15 The present invention is also directed to transgenic non-human mammals comprising recombinant DNA of the present invention with especially preferred transgenic mammals being mice and rats, said transgenic mammals exhibiting a diabetic phenotype.

20 In another embodiment, the present invention is directed to a method for treating an animal having disease characterized by an over expression of an IAPP gene product comprising,

administering a therapeutically-effective amount of an inhibitor of the over expression of said IAPP gene product to said mammal.

25 In yet another embodiment, the present invention is directed to a method of evaluating the effect of a treatment comprising administering said treatment and evaluating the effect of said treatment on the product of over expression of a gene encoding IAPP.

Preferred is the method wherein said treatment is administered to an animal with an especially preferred animal being a human.

30 The present invention is also directed to a method for determining if a subject is at risk for diabetes or obesity comprising examining said subject for the over expression of an IAPP gene product, said over expression being indicative of risk.

In still yet another embodiment, the present invention is directed to a method of evaluating an animal model for a disorder or disease comprising determining

if an IAPP gene in said animal model is expressed at a predetermined level with a preferred method being wherein said level is higher than the level in a wild type or normal animal.

Brief Description of the Drawings

5 Figure 1a is a linear map of the RIPHAT transgene. The human IAPP cDNA sequence is depicted in black; the rat insulin II promoter is depicted as a white box, the human albumin intron is a darkly shaded box, the human GAPDH polyadenylation region (labeled poly A) is depicted as a lightly shaded box.

10 Figure 1b is an enlargement of the ends of the coding region demonstrating the restriction sites that can be used to substitute alternative cDNAs for human IAPP.

Figure 1c is an enlargement of the ends of the promoter region demonstrating the restriction sites that can be used to substitute alternate promoters for RIP II in the RIPHAT transgene.

15 Figure 2 is a circular map of the plasmid pSV2Dog1. pSVDog1 was constructed by inserting the PCR-modified CAT gene (BspM I/BamH I fragment) downstream of the SV40 promoter (BamH I/Nco I partial fragment from pLuxF3). The resulting plasmid contains the CAT gene coding sequence fused at its 5' end with optimal mammalian translation sequences, and fused at its 3' end with the firefly luciferase 3'-untranslated region and poly A addition site. Expression of the modified CAT gene is driven by the
20 SV40 promoter.

Figure 3 is a circular map of the plasmid pSV2Dog11 containing the human glyceraldehyde 3 phosphate dehydrogenase polyadenylation region used to construct the plasmid pDog 15. pSV2Dog11 was constructed by inserting the PCR amplified human glyceraldehyde-3-phosphate dehydrogenase 3'-untranslated region into Spe I/BamH I digested pSV2Dog1. This places GAPDH 3' non-coding sequences downstream of the CAT coding region.

Figure 3 is a schematic drawing of the cloning strategy used to construct pRIPHAT1, starting with plasmid pDog15.

30 Figure 4 is an autoradiogram of a genomic DNA southern blot of 6 tail DNAs digested with the restriction endonuclease EcoRI and hybridized to the ³²P-labelled human GAPDH fragment within the RIPHAT transgene DNA. The 6 lanes represent a litter of animals produced from a cross of RIPHAT transgenic line RG male and FVB/N wild type female.

Figure 5 is an autoradiogram of a northern blot of total pancreatic RNA isolated from the transgenic lines RHA, RHF and RHG in addition to pancreatic RNA from Human Pancreas and a nontransgenic mouse. The blot was hybridized to a human IAPP cDNA fragment labelled with [alpha ³²P]dCTP.

5 Figure 6 is an electron micrograph of a pancreatic β cell. The arrows outline an intracellular amyloid plaque deposit.

Figure 7 is an electron micrograph showing a 37,000 fold magnification of immunogold staining of intracellular amyloid plaque by means of a rabbit anti human IAPP antibody.

10 Figure 8 is a graphical representation of the appearance of hyperglycemia in 3 male RHF homozygous mice compared to 3 nontransgenic (FVB/N strain) male mice.

Figure 9 depicts the results of an oral glucose tolerance test performed on 5 week old RHF homozygous transgenic males(litter # RHF11, n= 5) and females (litter # RHF11, n= 3) compared to age-matched nontransgenic FVB/N mice.

15 Detailed Description of the Invention

The Plasmids:

Plasmid pRIPHAT I(rat insulin promoter human IAPP transgene) (SEQ. ID NO: 1) contains DNA fragments from 5 different sources, three from human genes, the fourth from rat and the fifth being a commercially available plasmid vector. They are the rat insulin II promoter (876 bp); (SEQ ID NO: 2) human IAPP coding sequence (278 bp) (SEQ ID NO: 3), human albumin intron I(720 bp) (SEQ ID NO: 4), and the human glyceraldehyde-3-phosphate dehydrogenase(GAPDH) gene's polyadenylation site and RNA termination region (546 bp) (SEQ ID NO: 5). The commercially available plasmid is Bluescript SK(-) (Stratagene, La Jolla, CA) (SEQ. ID NO: 6). Enzymatic manipulations of recombinant DNA, including ligations, restriction endonuclease digestions, DNA synthesis reactions, and transformations of *E. coli* were carried out according to well-established procedures as described in Sambrook, J., Fritsch, E.F. and Maniatis, T. **Molecular Cloning: A Laboratory Manual**. 2nd Ed. Cold Spring Harbor Laboratory Press, New York, 1989.

30 The human albumin intron I (SEQ ID NO: 4) and GAPDH gene fragments (SEQ ID NO: 5) were obtained from the plasmid pSV2Dog15 by digestion of this plasmid with Bam HI and ApaLI and isolation of the 1262 bp fragment containing these two regions. pSV2Dog15 was constructed by David Lloyd and John Thompson of Pfizer, Inc. They

generated the human albumin intron I sequence by polymerase chain reaction (PCR) amplification (Innis, M.A. et al. eds., *PCR Protocols*, Academic Press, New York 1990) of this portion of the albumin gene using human genomic DNA (obtained from Clontech, Palo Alto, CA) and DNA oligomers 18505.022 (sequence 5' 5 CCCTCTAGAAGCTTGCTGGCAAGGGAAAGAAAA 3') (SEQ ID NO: 8) and 18505.024 (sequence 5' GGGAGCTCTAGACTTCGTCGAGGTGCACGTAAGAA 3') (SEQ ID NO: 9). Since these oligomers included exogenous Xba I sites on their ends, the resulting PCR product was digested with Xba I and inserted into the compatible Spe I site in pSV2Dog11. This plasmid, constructed by David Lloyd, in turn already contained the 10 human GAPDH polyadenylation region. It was also generated by PCR cloning using human genomic DNA as the template and oligomers 18970.246 (sequence 5' CAAACCGGATCCGCCCTGACTTCCTCCACCTGTCAGC 3') (SEQ ID NO: 10) and 18970.244 (sequence 5' CACAACACTAGTGACCCCTGGACCACCAGCCCCAGC 3') (SEQ ID NO: 11) as the PCR primers. The PCR product generated in this manner was 15 digested with Spe I and Bam HI and inserted into SpeI/Bam HI digested pSV2Dog1 (see Figure 2).

The 1262 bp, Apa LI/Bam HI albumin intronI-GAPDH polyA region hybrid fragment was ligated to a 278 bp PCR-amplified DNA fragment containing the coding region for the preproIAPP protein product. This fragment was amplified by using an 20 IAPP cDNA (lambda phage DNA hIAPP-c1, obtained from Sietse Mosseman, Rijksuniversiteit te Utrecht, The Netherlands and described in Mosseman, S. et al., Febs Lett. 247, 154-158 [1989]) as the template and oligomers 19383.288 (sequence 5' GTCATGTGCACCTAAAGGGGCAAGTAATTCA 3') (SEQ ID NO: 12) and 19987.116 (sequence 5' GAAGCCATGGGCATCCTGAAGCTGCAAGTA 3') (SEQ ID NO: 13) as the 25 PCR primers. The resulting 1523 bp fragment was ligated to pSuperLuc (pSL) to generate plasmid pSLA10. pSL is a DNA plasmid containing the luciferase reporter gene (Mosseman, S. et al. FEBS Lett. 271, 33-36 [1990]). In this case, the plasmid was used only for the presence of convenient Nco I and Bam HI restriction sites.

The rat insulin II promoter (SEQ ID NO: 2) and 5' untranslated leader region 30 were generated by PCR amplification of rat genomic DNA (obtained from Clontech, cat # 6750-1) using oligomers 19383.284 (sequence 5' GTCAGGAATTGGATCCCCAACCAACTCCAA-GT 3') (SEQ ID NO: 14) and 19383.292 (sequence 5' ACAGGGCCATGGTGGAACAAATGA-CCTGGAAAGATA 3') (SEQ ID NO: 15).

The oligomer 19383.292 contains a point mutation; and was so designed to introduce an Nco I site at the 3' end of the fragment by altering one nucleotide (A to C) 2 residues 5' of the initiation codon. The 883 bp PCR product was cleaved with Nco I to generate a 175 bp blunt end/Nco I fragment and a 708 bp fragment with 2 Nco I ends. The 5 plasmid pSLA 10 was digested with Xba I. The resulting 5' overhangs were filled in with Klenow polymerase and dNTPs to generate blunt ends. The plasmid was subsequently digested with Nco I and ligated to the 175 bp blunt end/Nco I rat insulin II fragment to generate pSLA11 (see Figure 3).

pSLA11 was digested with Nco I and ligated to the 708 bp Nco I rat insulin II 10 fragment to generate plasmid pSLA12. Proper orientation of the 708 bp Nco I fragment was confirmed by digestion of the plasmid with Eco RI and Bam HI. The chimeric transgene (rat insulin II promoter and 5' untranslated leader, IAPP coding region, albumin intron I, GAPDH polyadenylation region) (SEQ ID NO: 7) was transferred from the pSL backbone to Bam HI -linearized Bluescript SK(-) by partial Bam HI digestion of 15 pSLA12 to generate pRIPHAT 1 (SEQ ID NO: 1) . The rat insulin II promoter and 5' untranslated leader region and the IAPP coding region were sequenced by the dideoxy chain termination method of Sanger to ensure that no mutations were introduced.

To ensure that the transgene would be expressed in mouse cells, pRIPHAT 1 20 (SEQ ID NO: 1) was transiently transfected into β TC cells by means of electroporation as described by Mosselman et. al. (FEBS Lett. 271, 33-36. 1990). Total RNA was isolated by established methods (Chomczynski and Sachi, Anal. Biochem. 162, 156- 159) 24 hours later. The transgene-specific RNA was detected by PCR amplification of 25 the cDNA derived from this total RNA by reverse transcription (Innis, M.A. et al. eds., PCR Protocols, Academic Press, New York 1990). The size and abundance of the PCR product demonstrated that the transgene was expressed and that the human albumin intron portion of the transgene was efficiently spliced out in these cells.

The Stably Transfected Cell Lines

The above described plasmids were stably introduced into RIN and β TC3 cells 30 by electroporation along with a plasmid that confers geneticin(G418) resistance to the recipient cell. β TC3 cells were obtained from Shimon Efrat and Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., and are described in Efrat, S. et al. Proc. Natl. Acad. Sci. 85, 9037-9041 (1988). Cells were prepared for electroporation by trypsinization of semi-confluent monolayers, pelleting twice, 1 wash in serum-free RPMI

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1640 medium and resuspension in this medium at a concentration of 2×10^7 cells/ml. Routinely 50 μ g of the appropriate plasmid along with 3.3 μ g of the selection plasmid pH A2.3neo (confers G418 resistance; Dr. Peter Hobart, Pfizer, Inc.) were added to 0.5 ml of cells in an electroporation cuvette (Bethesda Research Labs [BRL], Gaithersburg, MD) and subjected to 250v/cm Field at 800 μ F and low resistance setting on a BRL Cell-Porator electroporation unit. The cells were allowed to rest for 2 minutes. They were then diluted with 2 volumes of RPMI 1640 10% fetal bovine serum and transferred to T25 flasks. After 36 hrs, viable cells were transferred to 6 well cluster dishes and grown at a concentration of 2×10^5 cells in selection medium (same as above with 500 μ g/ml active Geneticin). Colonies appeared after 3 weeks and they were isolated by established methods using trypsin and grease-coated porcelain cloning rings. Clones which survived this procedure were grown to mass culture, frozen and stored in liquid nitrogen. Confirmation of transgene expression was obtained by PCR amplification of cDNA derived from the clones' total RNA. In addition, a radioimmunoassay (Peninsula labs kit # RIK-7321, Belmont, CA) was performed on both total cell protein and surrounding medium to confirm both increased IAPP content and secretion.

Transgenic Mice.

Embryos from mouse strain FVB/N (Taketo, M. et al. Proc. Natl. Acad. Sci 88, 2065-2069 [1991]) were injected with linear DNA fragments that were isolated from the plasmid described above. The 2395 bp RIPHAT DNA fragment was released from its plasmid by cleavage with the Xba I and Xho I restriction endonucleases. The 2395 bp transgene fragment was isolated by electroelution (65V, 3 hrs.) after 2 rounds of agarose (0.9% GTG agarose, FMC Bioproducts, Rockland, Me) gel electrophoresis of the reaction digest. The fragment was further purified on a Schleicher and Schuell Elutip-d column following manufacturer's Elutip-d Basic Protocol for DNA purification prior to being injected into the embryos. Injection of the embryos was carried out according to published procedures, as outlined in Hogan, B. et al. **Manipulating the Mouse Embryo** Cold Spring Harbor Laboratories, New York, 1986.

Optimal Expression and Preferred Embodiments

The plasmids as described above can be altered to optimize expression of the transgene such as various insertions, deletions and/or single or multiple base pair substitutions. This includes single base pair alterations in the region in front of the initiation codon of luciferase to optimize translational efficiency. The promoter region

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within pRIPHAT 1 can be exchanged for other promoters, such as human IAPP, rat insulin I, mouse insulin, mouse IAPP, rat glucokinase(liver and /or β cell-specific), human gastrin, human or mouse albumin, mouse metallothionein and human tyrosine aminotransferase (Figure 1b). The rat insulin II promoter is depicted as a darkly shaded 5 box, the coding region as a black box, the human albumin intron as a white box and the human GAPDH polyadenylation region as a striped box. IAPP cDNAs of other species such as mouse, or mutated functional forms of human IAPP that retain either the amyloidogenic portions or the portions that induce insulin resistance, can be substituted for the human IAPP cDNA region within pRIPHAT1 (Figure 1c). The 10 transgene DNAs can be injected into other mouse strain embryos and mutants thereof, including db/+, Ob/+, A^w or A^v on either a C57BL/6J or C57BL/Ks background. Alternatively, these transgenic mice can be mated to strains with these genetic traits.

The preferred cell lines include β TC3 (Cold Spring Harbor Laboratories), RINm5f (Gazdar, A.F. et al. PNAS 77, 3519-3523 [1980] obtained from W. Chick, U. Mass., 15 Worcester, Massachusetts) and HIT (Santerre, R.F. et al. PNAS 78, 4339-4343 [1981]; obtained from ATCC Rockville MD).

Utility

The stably transfected cell lines can be used to screen drugs for their ability to alter transcription, mRNA levels, translation, accumulation or secretion of human IAPP. 20 In particular, steady state levels of transgene mRNA can be screened in a high throughput fashion using PCR detection methods. The cells can also be used to determine the mechanism of action of candidate drugs that are found to alter the above-mentioned processes.

The transgenic animals can be used to screen drugs for their ability to alter 25 human IAPP levels in cells, tissues, organs and/or plasma. They can also be used to study the pathological consequences of human IAPP overexpression in whole animals.

Experimental

Materials and Methods

Restriction enzymes including ApaLI, Bam HI, Hind III, Nco , Not I, Xba I, Xho 30 I and Eco RI were obtain d from N w England Biolabs. DNA modifying enzym s including T4 DNA Ligase and T4 DNA Kinase were obtained from the same source. Bact rial alkaline phosphatase was obtained from Boehringer Mannheim. All

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commercially obtained enzymes were utilized under conditions described as optimal by the supplier.

Media

The media for growth of *E. coli* consisted of 10 g Bacto-tryptone, 5 g Bacto-
5 yeast extract and 5 g NaCl. The pH was adjusted to 7.5 with 10N NaOH
after addition of all the ingredients.

Ethanol Precipitation of DNA

Sodium acetate(NaOAc) from a 3M, pH 5.2 stock solution was added to a DNA
sample to bring the final NaOAc concentration to 200 mM. Two and one-half volumes
10 of cold(-20°C) absolute ethanol were added to the one volume of aqueous DNA
sample and the sample placed at -70°C for 15 min. or -20°C overnight.

Electrophoresis of DNA

DNA in 10 mM Tris-HCl, pH 7.6 (or Hepes, pH 7.6) , 1 mM EDTA was mixed with
1/5 volume of Loading buffer. Loading Buffer consisted of 30% glycerol, 10 mM Tris-
15 HCl, pH 7.6, 20 mM ethylene diamine tetra acetic acid(EDTA), bromophenol blue.
0.25% (w/v)and xylene cyanol, 0.25% (w/v). DNA was electrophoresed through 0.8-1.2%
(w/v) GTG agarose (FMC Bioproducts, Rockland,ME) at 5-10 volts per cm of distance
between electrodes in 1X Tris-Borate EDTA (TBE) buffer (89 mM Tris, pH 8.3, 89 mM
Borate, 2 mM EDTA).

20 Electroelution of DNA

DNA bands were removed from gels by cutting out a gel slice containing the
band of interest with a clean single-edged razor blade and placing the gel slice in a
0.25 inch diameter dialysis tube (BRL Life Technologies, Inc., Gaithersburg, MD)(length
varying with size of gel slice) that was filled with 0.5X TBE buffer and subsequently
25 sealed on both ends with dialysis tube clips. The filled tube was placed in a standard
electrophoresis gel box filled with 0.5X TBE buffer and the DNA eluted out of the gel
slice onto the inner side of the dialysis tube by applying a voltage of 10 volts/cm of
distance between electrodes for 1-3 hours. At the end of this time the buffer solution
containing the DNA was transferred to an eppendorf tube, concentrated in a Speed-Vac
30 apparatus (Savant Instruments Inc. Farmingdale, N.Y.) to reduce the volume to a
minimum of 100 μ l. This volume was applied to a prepack d G-50 Sephadex
(Pharmacia, Piscataway, N.J.) spin column and centrifuged for 3 min. at 600 G force.in
an IEC tabletop clinical centrifuge (Int rnational Equipment Company, Needham HTS,

MA). This allowed removal of the borate salt from the DNA sample. The sample was then ethanol precipitated and resuspended in 10 mM Tris, pH 7.6 and 1 mM EDTA.

Visualization of DNA Bands in Gels

For DNA to be electrophoresed through agarose gels, 1/10 volume of a 1 mg/ml ethidium bromide (EtBr) solution was added to the sample. DNA bands were visualized after electrophoresis by placing the gel on a UV transilluminator emitting UV light at a wavelength of 320 nm. By this method no destaining procedure was required. DNA bands in gel slices isolated for preparative purposes were electroeluted as described above. The EtBr bound to the DNA was removed by the ethanol precipitation procedure.

Preparation of Bacterial Plasmid DNA

Maxiprep Procedure (for yields of 100 to 2000 μ gs of plasmid DNA).

This DNA was prepared by the alkaline lysis procedure described in Maniatis, Molecular Cloning: A Laboratory Manual. 0.5 liters of Luria broth, described under "Media" was inoculated with a 0.1 ml volume of a stationary phase culture of the appropriate E. coli strain.. After adding 125 μ g of dry ampicillin powder to the inoculated media, the bacteria were incubated at 37°C with shaking overnight. The next morning the bacteria were pelleted by centrifugation in a Sorvall GS3 rotor (Dupont Instrument Products, Biomedical Division, Newton, CT) at 5,000 rpm for 10 min at 4°C. The pelleted bacteria were resuspended in 20 ml of a solution consisting of 50 mM glucose, 25 mM Tris-HCl, pH 8.0, 10 mM EDTA and 5 mg/ml lysozyme. The bacteria were left at room temperature for 10 minutes, after which time 40 ml of 0.2 M NaOH/1% SDS was added. The lysed bacteria were allowed to sit at room temperature for an additional 10 minutes after which time we added 20 ml of ice cold 3M sodium acetate, pH 5.2, and the mixture incubated on ice for 10 min. The white precipitate was pelleted by centrifugation in the original tubes for 10 min. at 5,000 rpm in the GS3 rotor. The supernatant was collected and the volume measured. The DNA was precipitated by addition of one equal volume of isopropanol and pelleted by centrifugation in a Sorvall HSA rotor at 7,500 rpm for 15 minutes at 4°C. The pellet was dissolved in 2 ml of 10 mM Tris-HCl and added to a 5 ml polystyrene tube containing 3.10 gm of CsCl. The sample was transferred to a 3.9 ml Beckman heat seal tube containing 50 μ l of a 10 mg/ml solution of EtBr, filled with water, placed in a Beckmann TLN 100 rotor and centrifuged for 4 hours at 100,000 rpm.in an Optima TLX Beckman tabletop

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Ultracentrifuge (Beckman Instruments, Palo Alto, CA). Bands of plasmid DNA were visible to the naked eye and extracted with a 20G needle and 1cc tuberculin syringe. The EtBr was removed by extracting the plasmid solution with 3 M NaCl-saturated isopropanol. The DNA was subsequently ethanol-precipitated and stored at -20°C.

5 Miniprep Procedure(for yields of 1 to 20 μ gs of plasmid DNA)

This DNA was prepared by the boiling water procedure described in Maniatis, Molecular Cloning: A Laboratory Manual. 1.5 ml of a stationary culture of *E. coli* was poured into a 1.5 ml eppendorf tube. The remainder of the culture was stored at 4°C. The tube was centrifuged at 12,000 G for 15 seconds in an Eppendorf microfuge at 10 room temperature. The supernatant was removed by aspiration and the pellet resuspended in 0.4 ml of STET buffer: 8% sucrose, 0.5% Triton X100 detergent, 50 mM EDTA, 50 mM Tris-HCl, pH 8.0. 35 μ l of 10 mg/ml of lysozyme was added to the resuspended cells. The tube was immediately placed in 100°C water for 1 minute. The tube was removed from the boiling water and centrifuged for 15 minutes at 12,000G. 15 200 μ l of the supernatant was transferred to a new tube and mixed with 200 μ l of isopropanol. The sample was stored at -70°C for 15 minutes after which time the precipitated DNA was recovered by centrifugation at 12,000G at 4°C for 10 minutes. The DNA pellet was rinsed with 70% ethanol and allowed to air dry. The pellet was resuspended in 50 μ l of 10 mM Tris-HCl. pH 7.6 , 1mM EDTA and stored at 4°C.

20 Oral Glucose Tolerance Test

Mice to be tested were fasted for > 12 hours; blood samples were obtained from retro-orbital eye bleeds; blood glucose determinations were carried out by use of a "One Touch" Glucometer (Lifescan Inc., Milpitas CA). Blood sampling was carried out before administration of a glucose challenge($t = 0$), and 30, 75 and 120 minutes after 25 glucose challenge. The glucose challenge consisted of a 200 mg/ml dextrose solution administered orally at a 1mg/gm body weight dose by means of a 1cc syringe and murine oral dosing needle.

Bacterial plasmid DNA was prepared by the alkaline lysis method described in Maniatis, Molecular Cloning: A Laboratory Manual.

30 *E. coli* Transformation.

The bacterial strains consisted of either SURE cells obtained from Stratagene, Inc. or DH5 cells from Bethesda Research Labs, Gaithersburg, MD. Competent cells were prepared according to the CaCl₂ method (Maniatis et al. Molecular Cloning, Cold

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Spring Harbor Laboratories, 2nd Ed. 1989), flash frozen in liquid nitrogen and stored at -70°C. Transformation of these strains with plasmids of interest were typically carried out by incubation of 10 μ l of ligation mix with 80 μ l of competent cells followed by heat shock at 37°C for 2 min and subsequent incubation at 37°C for 1 hr after addition of 5 0.8 ml Luria broth. Typically, 100 μ l of this mixture was plated on LB plates containing 50 μ g/ml ampicillin as the selection agent. Colonies were picked after overnight incubation of the plate at 37°C.

Example 1: Construction of pRIPHAT

Construction of pSV2Dog15

10 A DNA fragment containing the human glyceraldehyde-3-phosphate dehydrogenase polyadenylation/ transcriptional termination region (SEQ ID NO: 5) was generated by polymerase chain reaction (PCR) amplification. The oligonucleotides 18970.244 (SEQ ID NO: 11) and 18970.246 (SEQ ID NO: 10) were incubated with 3 μ g of human genomic DNA (Clontech, SanCarlos, CA) under standard PCR conditions: 1 15 μ M primers, 3 μ g target DNA, 200 μ M dNTPs, 2.5 units Amplitaq DNA polymerase, 10 mM Tris-HCl, pH 8.3, 50 mM KCl, 1.5mM MgCl₂. The amplification conditions were set at 25 cycles, 1 min at 96°C, 2 min at 58°C, 3 min at 72°C. The resulting 545 bp fragment was digested with 10 units of Spe I and 10 units of Bam HI (37°C/30 min) and ligated to 1 μ g of phosphatased, SpeI/ Bam-digested vector DNA pSV2dog1 to 20 generate plasmid pSV2dog11. pSV2Dog11 itself was then digested with Spe I and treated with alkaline phosphatase (0.25 units from Boehringer Mannheim, in 50 mM TrisHCl, pH 8.5 at 55°C for 2 hours). A DNA fragment containing the human albumin 25 intron I (SEQ ID NO: 3) was generated by PCR amplification of 3 μ g of human genomic DNA (Clontech) utilizing oligonucleotides 18505.022 and 18505.024 under standard conditions described above. The resulting 740 bp fragment was digested with Spe I and ligated to Spe I -linearized pSV2 Dog11 under standard ligation conditions to 30 generate plasmid pSV2Dog15. The orientation of the intron fragment was confirmed by digestion of pSV2Dog15 with restriction endonuclease Aat I. 20 μ g of pSV2Dog15 was digested with 60 units of Bam HI and 22.5 units of Nco I to isolate a Nco I/BamH I fragment by electroelution. The micrograms of this fragment was subsequently digested with 20 units of Apa LI for 4 hrs. at 37°C. The resulting digestion products were separated on a 0.8% GTG agarose (FMC Bioproducts, Rockland, ME) gel. A 1265 bp Bam HI/Apa LI fragment was recovered by electroelution (standard conditions: 60

V/ 60 minutes in 0.5X TBE(Tris-borate-EDTA pH 8.3) with the gel slice in a dialysis bag). The eluted DNA was purified by spin column chromatography using G50 resin followed by ethanol precipitation. This fragment contained the human albumin intron fused on its 3' end to the human GAPDH polyadenylation region.

5 Construction of pSLA10

A portion of the human IAPP cDNA (SEQ ID NO: 2) containing only the protein coding region of the IAPP message was generated by PCR. Oligonucleotides 19383.288 (SEQ ID NO: 12) and 19383.292 (SEQ ID NO: 15), at a concentration of 1 uM were incubated with 0.1 ng cloned IAPP cDNA Hsiapp1 (Mosselman et al.) as the 10 template. Standard buffer and cycling conditions, as described above, were utilized. The reaction products were extracted with chloroform to remove residual mineral oil and ethanol precipitated. The precipitated DNA was resuspended in 20 ul of 1X NEB 4 restriction endonuclease buffer and 10 units of restriction endonuclease Apa LI. The digestion products were electrophoresed in a 1% GTG agarose gel, visualized by 15 ethidium bromide staining, and recovered by electroelution with a yield of 1.1 ug. This fragment was ligated to the BamHI/Apa LI, 1265 bp fragment from pSV2Dog15 in a total volume of 20 ul in 1X BRL ligation buffer plus units T4 DNA Ligase. The reaction was incubated at 16 C for 3 days. The residual ligase activity present in this reaction after this incubation was heat-inactivated (65°C/10 min.). This ligation reaction was then 20 diluted to 100 ul in the presence of high salt restriction buffer (100 mM NaCl, 10 mM Tris, pH 7.6, 10 mM MgCl₂) and digested with 5 units of Nco I for 2 hrs. at 37°C. The resultant fragment (1533 bp) was isolated by electrophoresis followed by electroelution.

The shuttle vector for cloning this fragment was prepared by digestion of 20 ug of the reporter plasmid pSuperluc (pSL) with 9 units of Nco I and 20 units of Bam HI 25 at 37°C for 3 hrs. in a reaction volume of 100 ul. To this reaction, 5 ul of 1M Tris, pH 8.0 and 22 units of alkaline phosphatase were added. The reaction was now allowed to proceed at 50°C for 2 hrs. to remove phosphate groups on the 5' overhangs and thus prevent recircularization of the vector alone in subsequent ligation steps. The phosphatase reaction was terminated by phenol/chloroform extraction followed by 30 ethanol precipitation. The DNA was resuspended in 10 mM Hepes, pH 7.6, 1 mM EDTA (HE) at a concentration of 0.2 ug/ul.

The 1533 bp IAPP cDNA/albumin intron/GAPDH polyA fragm nt was cloned into Nco I/ Bam HI-cut pSL by ligation of 1.1 ug of the insert to 0.2 ug of the pSL vector in

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a volume of 20 ul in 1X BRL ligation buffer and 400 units of T4 DNA Ligase. The reaction was incubated at 16°C overnight. On the following morning, competent *E. coli* SURE cells (Stratagene, San Diego, CA) were incubated with 10 ul of ligation mix at 0°C for 20 min followed by a 2 min heat shock at 37°C. 0.8 ml of Luria Broth were 5 added to the mix and incubated at 37°C for 60 min. 100 ul of this mix were spread onto a Luria Broth Agar plate containing 200 ug/ml ampicillin. Sixteen ampicillin-resistant colonies were picked and cultured in liquid broth; half of these cultures harbored plasmids with the proper insert as determined by digestion of miniprep DNAs (as described in Materials and Methods). One culture (miniprep #3) was grown up to 10 0.5 liter in Luria Broth for a NDA maxiprep and its plasmid was designated pSLA10.

Construction of pSLA11

The next step involved the insertion of the rat insulin II promoter (RIP) (SEQ ID NO: 2) into pSLA10. Because RIP contains an internal Nco I site, this process was carried out in 2 stages. The RIP DNA fragment itself (876 bp: 700 bp of 5' flank plus 15 176 bp of 5' untranslated leader including the first intron) was synthesized by PCR under standard conditions (above) utilizing 1 uM each of oligonucleotides 19383.284 (SEQ ID NO: 14) and 19383.292 (SEQ ID NO: 15); 3 ug of rat genomic DNA (Clontech) was used as the template. Oligonucleotide 19383.292 contains a single base alteration (A to C) 2 nucleotides 5' of the initiation codon in order to allow ligation of RIP to the 20 IAPP coding region via a Nco I site. The PCR product was chloroform extracted and ethanol precipitated. The DNA was resuspended in 20 ul of 1X NEB (New England Biolabs) 4 restriction buffer along with 5 units of Nco I and incubated at 37°C for 2 hrs. Two DNA fragments were recovered from this digestion by electrophoresis through 1.0% GTG agarose, visualization by ethidium bromide staining and electroelution of the 25 DNA from the gel slices: a 708 bp DNA with 2 Nco I ends containing the transcriptional start site and 5' leader region and a 168 bp blunt end/Nco I fragment containing the 5' most flanking sequence of the rat insulin II promoter.

The plasmid pSLA10 was first cleaved with Xba I. Ten micrograms of pSLA10 was digested with 20 units of Xba I in a volume of 100 ul of 1X high salt restriction 30 buffer (100 mM NaCl, 10 mM Tris, pH 7.6, 10 mM MgCl₂) for 2 hrs. at 37°C. The reaction was stopped by phenol/chloroform extraction followed by ethanol precipitation. The 5' single strand DNA overhangs were filled in by a polymerization step: the DNA was resuspended in 10 ul of 10 mM Hepes, pH 7.6, 1 mM EDTA and added to a final

reaction volume of 100 ul containing 10 mM Tris, pH 7.6, 10 mM MgCl₂, 50 mM NaCl, 5 units of Klenow enzyme and 25 uM dNTPs. This reaction was allowed to proceed at room temperature overnight. On the following morning, the fill-in reaction was heated at 65°C for 10 min to inactivate the Klenow enzyme; afterwards 2 ul of 5M NaCl and 5 units of restriction endonuclease Nco I were added and the reaction allowed to proceed at 37°C for 2 hrs. The cleavage reaction was stopped by the addition of 20 ul of gel loading buffer; consisting of 30% glycerol, 10 mM Tris-HCl, pH 7.6, 20 mM ethylene diamine tetra acetic acid (EDTA), bromophenol blue; 0.25% (w/v) xylene cyanol, 0.25% (w/v), the resulting mix was electrophoresed through a 0.8% GTG agarose gel. The linear form of the digested pSLA10 plasmid was recovered by electroelution followed by centrifugation through a G-50 spin column and ethanol precipitation. The precipitated DNA was resuspended in 10 ul of 10 mM Hepes, pH7.6, 1 mM EDTA. Two microliters (1 ug) of this solution was incubated with 0.25 ug of the 174 bp blunt end/Nco I fragment of the rat insulin promoter, 5 units of NEB T4 DNA ligase and 1X BRL (Bethesda Research Laboratories) ligation buffer in a final volume of 20 ul and incubated at 16°C overnight. The next morning 10 ul of the ligation reaction were used to transform competent *E. coli* SURE cells. Miniprep DNA was prepared (as described in Materials and Methods) from cultures of 16 colonies; 2 displayed Bam HI fragments of the correct size. One of these clones was grown as a DNA maxiprep as described in the Materials and Methods for preparation of more plasmid DNA and given the designation pSLA11.

pSLA11 was incubated with 7.5 units of Nco I in a volume of 200 ul in 1X NEB4 buffer at 37°C for 2 hrs. followed by the addition of 10 ul of 1mM Tris pH 8.0 and 22 units of Boehringer Mannheim alkaline phosphatase and further incubation at 50°C for 2 hrs. This was followed by 3 sequential phenol/chloroform extractions and ethanol precipitation. 0.32 ug of this linearized form of pSLA11 was ligated to 0.5 ug of the 760 bp Nco I rat insulin II promoter fragment described above in a volume of 20 ul in 1X BRL ligation buffer containing 20 units of NEB T4 DNA ligase; the reaction was incubated at 16°C overnight. Ten microliters of this ligation reaction were used to transform competent *E. coli* SURE cells (as described in Maniatis, Molecular Cloning: A Laboratory Manual). Of 8 colonies that arose from this transformation event, one miniprep DNA preparation displayed the correctly sized bands as determined by comparison to DNA molecular weight markers supplied by Bethesda Research

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Laboratories, Bethesda, MD, when digested with restriction endonuclease Eco RI. This plasmid was partially digested with Bam HI and the transgene insert, 2.4 kb in length, was ligated to Bam HI-digested Bluescript SK(-); generating pRIPHAT (SEQ. ID NO: 1)) in order to facilitate DNA sequence determination. One of 5 independently derived 5 clones displayed no inappropriate mutations and was used to prepare transgene insert for microinjection.

Preparation of RIPHAT DNA for Microinjection

Three hundred micrograms of pRIPHAT (SEQ. ID NO: 1) were digested with 300 units each of restriction endonucleases Xba I and Xho I in a total reaction volume of 10 600 ul at 37°C for 2 hrs. The reaction was stopped by the addition of EDTA to a concentration of 21 mM, followed by the addition of loading buffer and 2 rounds of electrophoresis through a 0.5 % GTG agarose gel. The gel slice containing the 2.4 kb DNA fragment was removed and the DNA isolated by electroelution (65V, 3 hrs.). The RIPHAT transgene fragment (2.4 kb (SEQ. ID. NO: 7)) was further purified utilizing a 15 Schleicher and Schuell Elutip-d column and following the manufacturer's protocol. The yield was 5.6 ug of purified RIPHAT fragment. pRIPHAT1 was deposited with the American Type Culture Collection on April 27, 1995 and received the designation ATCC 69794. This DNA was delivered to the Pfizer transgenic facility for microinjection.

Microinjection of Mouse Embryos and Generation of Transgenic Mice

20 The microinjection of mouse embryos and generation of transgenic mice was carried out by published procedures. Detailed procedures describing the preparation of mice, the microinjection procedure, the reimplantation of injected embryos, the maintenance of foster mothers, and the recovery and maintenance of transgenic lines can be found in Gordon, J and Ruddle, F., *Methods in Enzymology* 101, 411-433 (1983).
25 Embryos were isolated from female F1 progeny of strain FVB/N inbred crosses. The actual injection procedure was carried out as described in Wagner, T. et al. *PNAS* 78, 6376-6380 (1981) except that injected eggs were transferred immediately to donor females instead of 5 day incubations in culture tubes. Mice resulting from the reimplantation events were tested for presence of the transgene in their genomic DNA 30 by slot/Southern blotting of DNA isolated from tail biopsies. Those testing positive were crossed to nontransgenic FVB/N mice of the opposite sex. Offspring of these crosses were tested for transmission of the transgene by obtaining tail biopsies, isolating genomic DNA from them and PCR amplifying transgene sequences using primers

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22018-134-1 (5'-CGAGTGGGCTATGGGTTGT-3') (SEQ ID NO: 16) and 22018-134-2 (5'-GTCATGTGCACCTAAAGGGGCAAGTAATTCA-3') (SEQ ID NO: 17) to generate a diagnostic 883 bp PCR DNA product.

Establishment of Transgenic Lines

5 Those offspring testing positive for presence of the transgene were backcrossed to FVB/N mice for establishment of transgenic lines. Injection of 280 FVB/N embryos resulted in generation of 10 RIPHAT founders. Six of these founders were able to transmit the transgene to their offspring, as determined by PCR amplification of transgene sequences from genomic DNA isolated from offspring tail biopsies.

10 Identification of Lines Expressing the Transgene

Total RNA was prepared from various tissues of offspring from the 6 lines (including pancreas, liver and kidney). The RNA was isolated by polytron (Brinkmann Instruments, Westbury, N.Y.) homogenization of each of the tissues in 2 ml of TRISOLV™ (Biotecx Laboratories, Houston, TX) denaturant for 60 seconds. Addition 15 of 4 ml of chloroform allowed separation of the homogenate into an upper, aqueous phase and a lower phenol/chloroform phase. The RNA was precipitated by addition of an equal volume of isopropanol to the aqueous phase of each homogenate. The isopropanol precipitates were centrifuged at 12,000 G for 10 min at 4°C, washed once with 75% ethanol and allowed to air dry. The RNA samples were resuspended in 200 20 µl of 1 mM EDTA and their concentration determined by UV spectrophotometry. Northern analysis was carried out as described in Maniatis, utilizing 1.0% GTG formaldehyde agarose gels, blotting to Nylon membranes and hybridizing the blot to a ³²P-labelled DNA fragment that corresponds to the human GAPDH polyadenylation region within the RIPHAT transgene. RIPHAT-specific RNA was detected in lines RHA, 25 RHF and RHC, with lines RHA and RHF displaying 10 fold higher pancreatic expression than line RHC. Line RHF was selected for colony expansion.

Generation of Line RHF Homozygotes

The transgenic hemizygous RHF offspring were subjected to brother-sister matings to generate nontransgenic to hemizygote to homozygote offspring in a 1:2:1 30 ratio. Transgenic offspring were identified by PCR analysis of tail biopsies; homozygotes within this group were identified by test-crossing the transgenics to wild-type FVB/N mates and identifying those animals that would generate no nontransgenic

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offspring (>20 offspring per putative homozygote). Homozygotes that were identified in this manner were intercrossed to generate a colony of RHF homozygotes.

Determination of Plasma IAPP and Insulin Levels

Representative nontransgenic littermates, hemizygous and homozygous animals 5 were sacrificed by CO₂ asphyxiation. Whole blood was obtained from Vena Cava puncture of asphyxiated animals with a 20G needle and 1 ml tuberculin syringe. The whole blood was transferred to 1.0 ml Microtainer Plasma separator tubes (Becton Dickinson, Rutherford, NJ) to prevent coagulation and centrifuged at 2000G for 2 min to allow plasma isolation. The plasmas were quick frozen in dry ice and stored at 10 -70°C until assayed.

Use of Line RHF Homozygotes for Drug Screening

Typically, animals are divided into groups of 10 for each dose of a given test compound. Their plasma glucose levels are determined by retro-orbital eye bleeds on day 1 before dosing. Dosing is carried out daily, e.g., at 0.1, 1.0 and 10 mg/kg, for 15 days 1 through 4. On day 5 the animals are bled to determine their fasting plasma glucose levels with the aim of detecting a glucose lowering effect. Alternatively, the animals are subjected to an oral glucose tolerance test (OGTT) to demonstrate improved glucose tolerance. The animals are then exsanguinated in order to measure plasma insulin levels and demonstrate a drop in insulin concentration.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

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Carty, Maynard D.
5 Kreutter, David K.

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(APPLICANT FOR ALL OTHER COUNTRIES)

10 (ii) TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II
DIABETES MELLITUS

(iii) NUMBER OF SEQUENCES: 17

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(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10017-5755

(v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

25 (A) APPLICATION NUMBER: US N/A
(B) FILING DATE:
(C) CLASSIFICATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5356 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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	GCGGTATCAG	CTCACTCAAA	GGCGGTAAATA	CGGTTATCCA	CAGAATCAGG	GGATAACGCA	3540
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	TCCGGTA	ACT ATCGTCTTGA	GTCCAACCCG	GTAAGACACG	ACTTATCGCC	ACTGGCAGCA	3960
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	CCCGTCGTGT	AGATAACTAC	GATA CGGGAG	GGCTTACCAT	CTGGCCCCAG	TGCTGCAATG	4500
	ATACCGCGAG	ACCCACCGCTC	ACCGGCTCCA	GATTATCAG	CAATAAACCA	GCCAGCCGGA	4560
35	AGGGCCGAGC	GCAGAAGTGG	TCCTGCAACT	TTATCCGCCT	CCATCCAGTC	TATTAATTGT	4620
	TGCCGGGAAG	CTAGAGTAAG	TAGTCGCCA	GTAAATAGTT	TGCGCAACGT	TGTTGCCATT	4680
	GCTACAGGCA	TCGTGGTGT	ACGCTCGTC	TTTGGTATGG	CTTCATTCA	CTCCGGTTCC	4740
	CAACGATCAA	GGCGAGTTAC	ATGATCCCC	ATGTTGTGCA	AAAAAGCGGT	TAGCTCCCTC	4800
	GGTCCCTCCGA	TCGTTGTCA	AGTAAGTTG	GCCGCAGTGT	TATCACTCAT	GGTTATGGCA	4860
40	GCACTGCATA	ATTCTCTTAC	TGTCATGCCA	TCCGTAAGAT	GCTTTCTGT	GACTGGTGA	4920
	TACTCAACCA	AGTCATTCTG	AGAATAGTGT	ATGCGGCAC	CGAGTTGCTC	TTGCCCGGCG	4980
	TCAATACGGG	ATAATACCGC	GCCACATAGC	AGAACTTAA	AAAGTGTCA	CATTGGAAAA	5040
	CGTTCTCGG	GGCGAAA	ACT CTCAAGGATC	TTACCGCTGT	TGAGATCCAG	TTCGATGTAA	5100

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	CCCACTCGTG CACCCAACTG ATCTTCAGCA TCTTTACTT TCACCAGCGT TTCTGGGTGA	5160
	GCAAAAACAG GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA	5220
	ATACTCATAAC TCTTCCTTT TCAATATTAT TGAAGCATT ATCAGGGTTA TTGTCTCATG	5280
	AGCGGATACA TATTGAATG TATTTAGAAA AATAAACAAA TAGGGGTTCC GCGCACATTT	5340
5	CCCCGAAAAG TGCCAC	5356
	(2) INFORMATION FOR SEQ ID NO:2:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 876 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
15	GGATCCCCCA ACCACTCCAA GTGGAGGCTG AGAAAGGTTT TGTAGCTGGG TAGAGTATGT	60
	ACTAAGAGAT GGAGACAGCT GGCTCTGAGC TCTGAAGCAA GCACCTCTTA TGGAGAGTTG	120
	CTGACCTTCA GGTGCAAATC TAAGATACTA CAGGAGAATA CACCATGGGG CTTCAAGCCCCA	180
	GTGACTCCC GAGTGGGCTA TGGGTTTGTG GAAGGAGAGA TAGAAGAGAA GGGACCTTTC	240
	TTCTTGAATT CTGCTTCCT TCTACCTCTG AGGGTGAGCT GGGGTCTCAG CTGAGGTGAG	300
20	GACACAGCTA TCAGTGGGAA CTGTGAAACA ACAGTTCAAG GGACAAAGTT ACTAGGTCCC	360
	CCAACAACTG CAGCCCTCTG GGGAAATGATG TGGAAAAATG CTCAGCCAAG GACAAAGAAG	420
	GCCTCACCCCT CTCTGAGACA ATGTCCCCCTG CTGTGAACCTG GTTCATCAGG CCACCCAGGA	480
	GCCCCCTATTA AGACTCTAAT TACCTAAGG CTAAGTAGAG GTGTTGTGT CCAATGAGCA	540
	CTTCTGCAG ACCTAGCACC AGGCAAGTGT TTGGAAACTG CAGCTTCAGC CCCCTCTGGCC	600
25	ATCTGCTGAT CCACCCTTAA TGGGACAAAC AGCAAAGTCC AGGGGTCAGG GGGGGGTGCT	660
	TTGGACTATA AAGCTAGTGG GGATTCAAGTA ACCCCCCAGCC CTAAGTGACC AGCTACAGTC	720
	GGAAACCATC AGCAAGCAGG TATGTACTCT CCAGGGTGGG CCTGGCTTCC CCAGTCAGCA	780
	CTCCAGGGAT TTGAGGGACG CTGTGGGCTC TTCTCTTACA TGTACCTTT GCTAGCCTCA	840
	ACCCCTGACTA TCTTCCAGGT CATTGTTCCA CCATGG	876
30	(2) INFORMATION FOR SEQ ID NO:3:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 278 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
	CCATGGGCAT CCTGAAGCTG CAAGTATTC TCATTGTGCT CTCTGTTGCA TTGAACCATC	60
	TGAAAGCTAC ACCCATTGAA AGTCATCAGG TGGAAAAGCG GAAATGCAAC ACTGCCACAT	120
40	GTGCAACGCCA GCGCCTGGCA AATTTTTAG TTCATTCCAG CAACAACCTT GGTGCCATTC	180
	TCTCATCTAC CAACGTGGGA TCCAATACAT ATGGCAAGAG GAATGCAGTA GAGGTTTAA	240
	AGAGAGAGCC ACTGAATTAC TTGCCCCCTT AGGTGCAC	278
	(2) INFORMATION FOR SEQ ID NO:4:	

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGCACGTAA GAAATCCATT TTTCTATTGT TCAACTTTA TTCTATTTTC CCAGTAAAAT	60
10 AAAGTTTAG TAAACTCTGC ATCTTAAAG AATTATTTG GCATTTATTT CTAAAATGGC	120
ATAGCATTTC GTATTTGTGA AGTCTTACAA GGTTATCTTA TTAATAAAAT TCAACACATCC	180
TAGGTAAAAA AAAAAGGTCA GAATTGTTA GTGACTGTAA TTTCTTTTG CGCACTAAGG	240
AAAGTGCAAA GTAACTTAGA GTGACTGAAA CTTCACAGAA TAGGGTTGAA GATTGAATTG	300
ATAACTATCC CAAAGACCTA TCCATTGCAC TATGCTTTAT TTAAAAACCA CAAAACCTGT	360
15 GCTGTTGATC TCATAAAATAG AACTTGTATT TATATTATTACATTTAG TCTGTCCTCT	420
TGGTTGCTGT TGATAGACAC TAAAAGAGTA TTAGATATTA TCTAAGTTG AATATAAGGC	480
TATAAAATATT TAATAATTTT TAAAATAGTA TTCTGGTAA TTGAATTATT CTTCTGTTA	540
AAGGCAGAAG AAATAATTGA ACATCATCCT GAGTTTTCT GTAGGAATCA GAGCCCAATA	600
TTTGAAACA AATGCATAAT CTAAGTCAAA TGGAAAGAAA TATAAAAAGT AACATTATTA	660
20 CTTCTGTTT TCTTCAGTAT TTAACAATCC TTTTTTTCT TCCCTTGCCC AGACAAGCTT	720

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTCTAG TGACCCCTGG ACCACCAGCC CCAGCAAGAG CACAAGAGGA AGAGAGAGAC	60
30 CCTCACTGCT GGGGAGTCCC TGCCACACTC AGTCCCCAC CACACTGAAT CTCCCCTCCT	120
CACAGTTGCC ATGTAGACCC CCTGAAGAGG GGAGGGGCCT AGGGAGCCGC ACCTTGTCAAT	180
GTACCATCAA TAAAGTACCC TGTGCTAAC CAGTTACTTG TCCTGTCTTA TTCTAGGGTC	240
TGGGGCAGAG GGGAGGGAAG CTGGGCTTGT GTCAAGGTGA GACATTCTG CTGGGGAGGG	300
ACCTGGTATG TTCTCCTCAG ACTGAGGGTA GGGCCTCCAA ACAGCCTTGC TTGCTTCGAG	360
35 AACCATTTGC TTCCCGCTCA GACGTCTTGA GTGCTACAGG AAGCTGGCAC CACTACTCA	420
GAGAACAAAGG CCTTTTCCCTC TCCTCGCTCC AGTCCTAGGC TATCTGCTGT TGGCAAACA	480
TGGAAAGAAGC TATTCTGTGG GCAGCTCCAG GGAGGCTGAC AGGTGGAGGA AGTCAGGGCG	540
GATCC	545

(2) INFORMATION FOR SEQ ID NO:6:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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	(D) TOPOLOGY: circular	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
	CTGACGCGCC CTGTAGCGGC GCATTAAGCG CGGCAGGTGT GGTGGTTACG CGCAGCGTGA	60
5	CCGCTACACT TGCCAGCGCC CTAGCGCCCG CTCCCTTCGC TTTCTTCCCT TCCTTTCTCG	120
	CCACGTTCGC CGGCTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTA GGGTTCCGAT	180
	TTAGTGCTTT ACGGCACCTC GACCCCAAAA AACTTGATTA GGGTGATGGT TCACGTAGTG	240
	GGCCATCGCC CTGATAGACG GTTTTCGCC CTTTGACGTT GGAGTCCACG TTCTTTAATA	300
	GTGGACTCTT GTTCCAAACT GGAACAAACAC TCAACCCAT CTCGGTCTAT TCCTTGATT	360
10	TATAAGGGAT TTTGCCGATT TCGGCCTATT GGTTAAAAAA TGAGCTGATT TAACAAAAAT	420
	TTAACGCAGAA TTTTAACAAA ATATTAACGC TTACAATTTC CATTGCCAT TCAGGCTGCG	480
	CAACTGTTGG GAAAGGGCGAT CGGTGCGGGC CTCTTCGCTA TTACGCCAGC TGGCGAAAGG	540
	GGGATGTGCT GCAAGGGCGAT TAAAGTGGGT AACGCCAGGG TTTTCCCAGT CACGACGTTG	600
	TAAAACGACG GCCAGTGAGC GCGCGTAATA CGACTCACTA TAGGGCGAAT TGGGTACCGG	660
15	GCCCCCCCCTC GAGGTGACG GTATCGATAA GCTTGATATC GAATTCCCTGC AGCCCCGGGG	720
	ATCCACTAGT TCTAGAGCGG CCGCCACCGC GGTGGAGCTC CAGCTTTGT TCCCTTTAGT	780
	GAGGGTTAAT TGCGCGCTTG GCGTAATCAT GGTCTAGCT GTTTCCTGTG TGAAATTGTT	840
	ATCCGCTCAC AATTCCACAC AACATACGAG CCGGAAGCAT AAAGTGTAAA GCCTGGGGTG	900
	CCTAATGAGT GAGCTAACTC ACATTAATTG CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG	960
20	GAAACCTGTC GTGCCAGCTG CATTAATGAA TCGGCCAACG CGCGGGGAGA GGCGGTTTGC	1020
	GTATTGGCGC CTCTTCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTG GTTCCGGCTGC	1080
	GGCGAGCGGT ATCAGCTCAC TCAAAGGCAGG TAATACGGTT ATCCACAGAA TCAGGGATA	1140
	ACCGCAGGAAA GAACATGTGA GCAAAAGGCC AGCAAAAGGC CAGGAACCGT AAAAGGCCG	1200
	CGTTGCTGGC GTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCCACGCT	1260
25	CAACTCAGAG GTGGCGAAC CCGACAGGAC TATAAAGATA CCAGGCCTT CCCCCCTGGAA	1320
	GCTCCCTCGT GCGCTCTCCT GTTCCGACCC TGCCGCTTAC CGGATACCTG TCCGCCCTTC	1380
	TCCCTTCGGG AAGCGTGGCG CTTTCTCATA GCTCACGCTG TAGGTATCTC AGTTCGGTGT	1440
	AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC ACGAACCCCC CGTTCAGGCC GACCGCTGCG	1500
	CCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG	1560
30	CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTTCT	1620
	TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT ATTTGGTATC TGCGCTCTGC	1680
	TGAAGCCAGT TACCTTCGGA AAAAGAGTTG GTAGCTCTTG ATCCGGCAA CAAACCACCG	1740
	CTGGTAGCGG TGTTTTTT GTTGCAAGC AGCAGATTAC GCGCAGAAAA AAAGGATCTC	1800
	AGGAAGATCC TTTGATCTTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT	1860
35	AAAGGGATTT GGTCTAGAGA TTATCAAAA GGATCTTCAC CTAGATCCTT TTAAATTAAA	1920
	AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAAT	1980
	GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT TCGTTCATCC ATAGTTGCCT	2040
	GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC CCCAGTGCTG	2100
	CAATGATACC GCGAGACCCA CGCTCACCGG CTCCAGATTT ATCAGCAATA AACCGCCAG	2160
40	CCGGAACGGGC CGACGCCAGA ACTGGTCCCTG CAACTTATC CGCCTCCATC CAGTCTATTA	2220
	ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTGCGC AACGTTGTTG	2280
	CCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTGG TATGGCTTCA TTCAGCTCCG	2340
	GTCCCCAACG ATCAAGGCCA GTTACATGAT CCCCCATGTT GTGCAAAAAA GCGGTTAGCT	2400

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	CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTATCA CTCATGGTTA	2460
	TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTT TCTGTGACTG	2520
	GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCC GCGACCGAGT TGCTCTTGCC	2580
	CGGGGTCAAT ACGGGATAAT ACCCGGCCAC ATAGCAGAAC TTTAAAAGTG CTCATCATTG	2640
5	GAAAACGTTC TTCGGGGCGA AAACTCTCAA GGATCTTACG GCTGTTGAGA TCCAGTTCGA	2700
	TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTT TACTTTCACC AGCGTTCTG	2760
	GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAAGGG AATAAGGGCG ACACGGAAAT	2820
	GTTGAATACT CATACTCTTC CTTTTCAAT ATTATTGAAG CATTATCAG GGTTATTGTC	2880
	TCATGAGCGG ATACATATTT GAATGTATT AGAAAAATAA ACATAAGGG GTTCCCGCGCA	2940
10	CATTTCCCCG AAAAGTGCCA C	2961

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2395 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	GATCCCCCAA CCACTCCAAG TGGAGGCTGA GAAAGGTTT GTAGCTGGGT AGAGTATGTA	60
20	CTAAGAGATG GAGACAGCTG GCTCTGAGCT CTGAAGCAAG CACCTCTTAT GGAGAGTTGC	120
	TGACCTTCAG GTGCAAATCT AAGATACTAC AGGAGAAATAC ACCATGGGGC TTCAGGCCAG	180
	TTGACTCCCG AGTGGGCTAT GGGTTTGTGG AAGGAGAGAT AGAAGAGAAG GGACCTTTCT	240
	TCTTGAATTG TGCTTCCCTT CTACCTCTGA GGGTGAGCTG GGGTCTCAGC TGAGGTGAGG	300
	ACACAGCTAT CAGTGGGAAC TGTGAAACAA CAGTTCAAGG GACAAAGTTA CTAGGTCCCC	360
25	CAACAACCTGC AGCCTCCTGG GGAATGATGT GGAAAAATGC TCAGCCAAGG ACAAAAGAAGG	420
	CCTCACCCCTC TCTGAGACAA TGTCCCCCTGC TGTGAACCTGG TTCATCAGGC CACCCAGGAG	480
	CCCCTATTAA GACTCTAATT ACCCTAAGGC TAAGTAGAGG TGTGTTGTC CAATGAGCAC	540
	TTTCTGCAGA CCTAGCACCA GGCAGTGTGTT TGGAAACTGC AGCTTCAGCC CCTCTGGCCA	600
	TCTGCTGATC CACCCCTTAAT GGGACAAACA GCAAAGTCCA GGGGTCAAGGG GGGGGTGCTT	660
30	TGGACTATAA AGCTAGTGGG GATTCACTAA CCCCCAGCCC TAAGTGACCA GCTACAGTCG	720
	GAAACCATCA GCAAGCAGGT ATGTACTCTC CAGGGTGGGC CTGGCTTCCC CAGTCAGAC	780
	TCCAGGGATT TGAGGGACGC TGTGGGCTCT TCTCTTACAT GTACCTTTTG CTAGCCTCAA	840
	CCCTGACTAT CTTCCAGGTC ATTGTTCCAC CATGGGCATC CTGAAGCTGC AAGTATTCT	900
	CATTGTGCTC TCTGTTGCAT TGAACCCTCT GAAAGCTACA CCCATTGAAA GTCATCAGGT	960
35	GGAAAAGCGG AAATGCAACA CTGCCACATG TCCAACGCAG CGCCTGGCAA ATTTTTAGT	1020
	TCATTCCAGC AACAACTTTG GTGCCATTCT CTCATCTACC AACGTGGGAT CCAATACATA	1080
	TGGCAAGAGG AATGCAGTAG AGGTTTTAAA GAGAGAGCCA CTGAATTACT TGCCCTTTA	1140
	GGTGCACGTA AGAAATCCAT TTTTCTATTG TTCAACTTTT ATTCTATTTC CCCAGTAAA	1200
	TAAAGTTTA GTAAACTCTG CATCTTAAA GAATTATTGG GGCATTTATT TCTAAATGG	1260
40	CATAGCATTG TGTATTGTG AAGTCTTACA AGGTTATCTT ATTAATAAAA TTCAAACATC	1320
	CTAGGTAAAA AAAAAAGGTC AGAATTGTT AGTGACTGTA ATTTCTTTT GCGCACTAAG	1380
	GAAAGTGCAGA AGTAACCTAG AGTGACTGAA ACTTCACAGA ATAGGGTTGA AGATTGAATT	1440
	CATAACTATC CCAAAGACCT ATCCATTGCA CTATGTTTA TTTAAAAACC ACAAAACCTG	1500

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	TGCTGTTGAT CTCATAAATA GAACTTGTAT TTATATTTAT TTACATTTA GTCTGTCTTC	1560
	TTGGTTGCTG TTGATAGACA CTAAGAGAGT ATTAGATATT ATCTAAGTTT GAATATAAGG	1620
	CTATAAATAT TTAATAATT TAAAGAGT ATTCTGGTA ATTGAATTAT TCTTCTGTT	1680
	AAAGGCAGAA GAAATAATTG AACATCATCC TGAGTTTTC TGTAGGAATC AGAGCCCAAT	1740
5	ATTTGAAAC AAATGCATAA TCTAAGTCAA ATGGAAAGAA ATATAAAAAG TAACATTATT	1800
	ACTTCTGTT TTCTTCAGTA TTTAACAAATC CTTTTTTTC TTCCCTTGCC CAGACAAGCT	1860
	TCTAGTGACC CCTGGACAC CAGCCCCAGC AAGAGCACAA GAGGAAGAGA GAGACCCCTCA	1920
	CTGCTGGGGA GTCCCTGCCA CACTCAGTCC CCCACCACAC TGAATCTCCC CTCCCTCACAG	1980
	TTGCCATGTA GACCCCCCTGA AGAGGGGAGG GGCCTAGGGA GCCGCACCTT GTCATGTACC	2040
10	ATCAATAAAG TACCCCTGTGC TCAACCAGTT ACTTGTCCCTG TCTTATTCTA GGGTCTGGGG	2100
	CAGAGGGGAG GGAAGCTGGG CTTGTGTCAA GGTGAGACAT TCTTGCTGGG GAGGGACCTG	2160
	GTATGTTCTC CTCAGACTGA GGGTAGGGCC TCCAAACAGC CTTGCTTGCT TCGAGAACCA	2220
	TTTGCTTCCC GCTCAGACGT CTTGAGTGCT ACAGGAAGCT GGCACCACCA CTTCAGAGAA	2280
	CAAGGCCTTT TCCTCTCCTC GCTCCAGTCC TAGGCTATCT GCTGTTGCC AACATGGAA	2340
15	GAAGCTATTG TGTGGCAGC TCCAGGGAGG CTGACAGGTG GAGGAAGTCA GGGCG	2395
	(2) INFORMATION FOR SEQ ID NO:8:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 34 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
	CCCTCTAGAA GCTTGTCTGG GCAAGGGAAAG AAAA	34
25	(2) INFORMATION FOR SEQ ID NO:9:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 38 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
	GGGAAGCTTC TAGACTTCG TCGAGGTGCA CGTAAGAA	38
	(2) INFORMATION FOR SEQ ID NO:10:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 37 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
	CAAACCGGAT CCGCCCTGAC TTCCTCCACC TGTCAGC	37
	(2) INFORMATION FOR SEQ ID NO:11:	

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5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1
CACAAACACTA GTGACCCCTG GACCACCAGC CCCAGC

15 (2) INFORMATION FOR SEQ ID NO:12:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2
GTCATGTGCA CCTAAAGGGG CAAGTAATTCA

20 (2) INFORMATION FOR SEQ ID NO:13:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3
GAAGCCATGG GCATCCGTAA GCTGCAAGTA

25 (2) INFORMATION FOR SEQ ID NO:14:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4
GAAGCCATGG GCATCCGTAA GCTGCAAGTA

30 (2) INFORMATION FOR SEQ ID NO:15:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5
GTCAGGAATT CGGATCCCCC AACCACTCCA AGT

35 (2) INFORMATION FOR SEQ ID NO:16:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6
GTCAGGAATT CGGATCCCCC AACCACTCCA AGT

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
ACAGGGCCAT GGTGGAACAA TGACCTGGAA GATA 34

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
CGAGTGGGCT ATGGGTTTGT 20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

20 GTCATGTGCA CCTAAAGGGG CAAGTAATTC A 31

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CLAIMS

1. Recombinant DNA comprising a non-IAPP promoter, a sequence encoding human IAPP or an active fragment thereof functionally linked to a human albumin intron I encoding sequence, a human GAPDH termination encoding sequence and a human GAPDH polyadenylation encoding sequence, said DNA resulting in expression of a diabetic phenotype when incorporated into a suitable host.
2. Recombinant DNA according to claim 1 wherein the non-IAPP promoter is selected from the group consisting of promoters for the genes for rat insulin I, rat insulin II, human insulin, mouse IAPP, rat B cell-specific glucokinase, glucose transporter 2 human tyrosine amino transferase, human albumin, mouse albumin, rat liver specific glucokinase and mouse metallothionein.
3. Recombinant DNA according to claim 2 wherein said promoter is the rat insulin promoter II.
4. Recombinant DNA according to claim 1 wherein said sequence encoding human IAPP or an active fragment thereof has the characteristics of genomic DNA.
5. Recombinant DNA according to claim 5 wherein said sequence encoding human IAPP or of active fragment thereof has the characteristics of cDNA.
6. Recombinant DNA according to claim 1 wherein said sequence is that of SEQ ID NO: 1.
7. Recombinant DNA according to claim 5 wherein said sequence of cDNA is that of SEQ ID NO: 3.
8. Recombinant DNA according to claim 1 wherein the sequence encoding human IAPP is replaced by a sequence encoding mouse IAPP or an active fragment thereof.
9. Recombinant DNA according to claim 8 wherein said DNA is cDNA.
10. A vector comprising recombinant DNA according to claim 1.
11. A vector comprising recombinant DNA according to claim 4.
12. A vector comprising recombinant DNA according to claim 5.
13. An eukaryotic cell line comprising recombinant DNA according to claim 1.
14. An eukaryotic cell line comprising recombinant DNA according to claim 4.

15. An eukaryotic cell line comprising recombinant DNA according to claim 5.
16. A cell line according to claim 13 wherein the cells are selected from the group consisting of rat insulinoma (RIT) cells, rat insulinoma (HIT) cells and β -TC3 mouse insulinoma cells.
17. A cell line according to claim 14 wherein the cells are selected from the group consisting of rat insulinoma (RIT) cells, rat insulinoma (HIT) cells and β -TC3 mouse insulinoma cells.
18. A cell line according to claim 13 wherein the cells are selected from the group consisting of rat insulinoma (RIT) cells, rat insulinoma (HIT) cells and β -TC3 mouse insulinoma cells.
19. A transgenic non-human mammal comprising recombinant DNA according to claim 1.
20. A transgenic non-human mammal comprising recombinant DNA according to claim 4.
21. A transgenic non-human mammal comprising recombinant DNA according to claim 5.
22. A transgenic non-human mammal according to claim 19 wherein said animal is a mouse.
23. A transgenic non-human mammal according to claim 20 wherein said animal is a mouse.
24. A transgenic non-human mammal according to claim 21 wherein said animal is a mouse.
25. A method for treating an animal having disease characterized by an over expression of an IAPP gene product comprising, administering a therapeutically-effective amount of an inhibitor of the over expression of said IAPP gene product to said mammal.
26. A method of evaluating the effect of a treatment comprising administering said treatment and evaluating the effect of said treatment on the product of over expression of a gene encoding IAPP.
27. The method of claim 26, wherein said treatment is administered to an animal.
28. The method of claim 27 wherein said animal is a human.

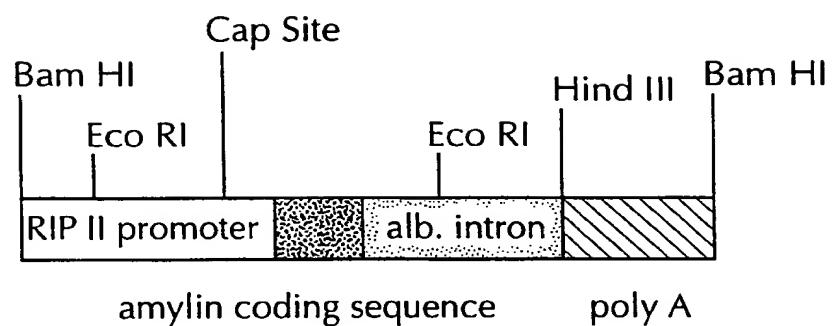
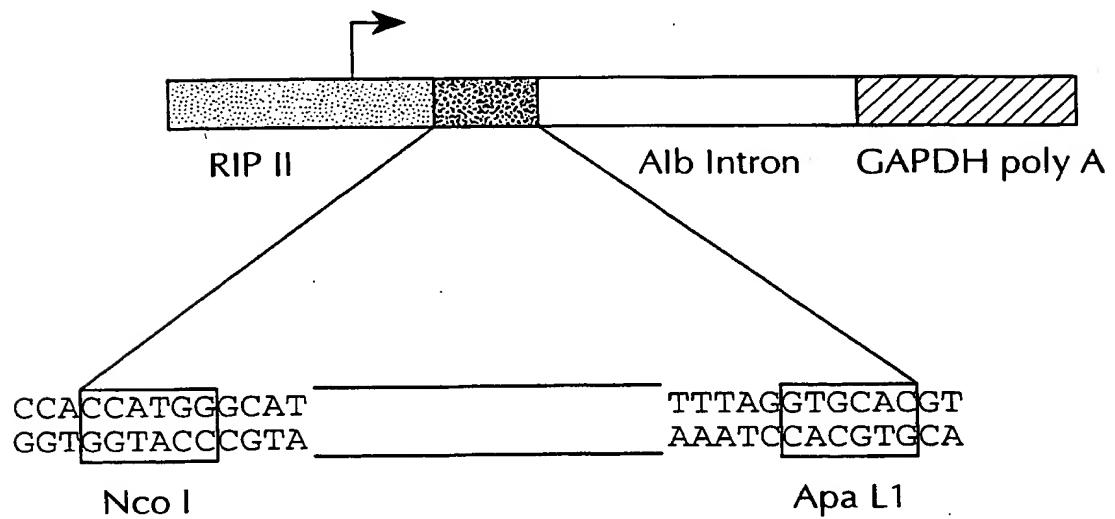
-32-

29. A method for determining if a subject is at risk for diabetes or obesity comprising examining said subject for the over expression of an IAPP gene product, said over expression being indicative of risk.

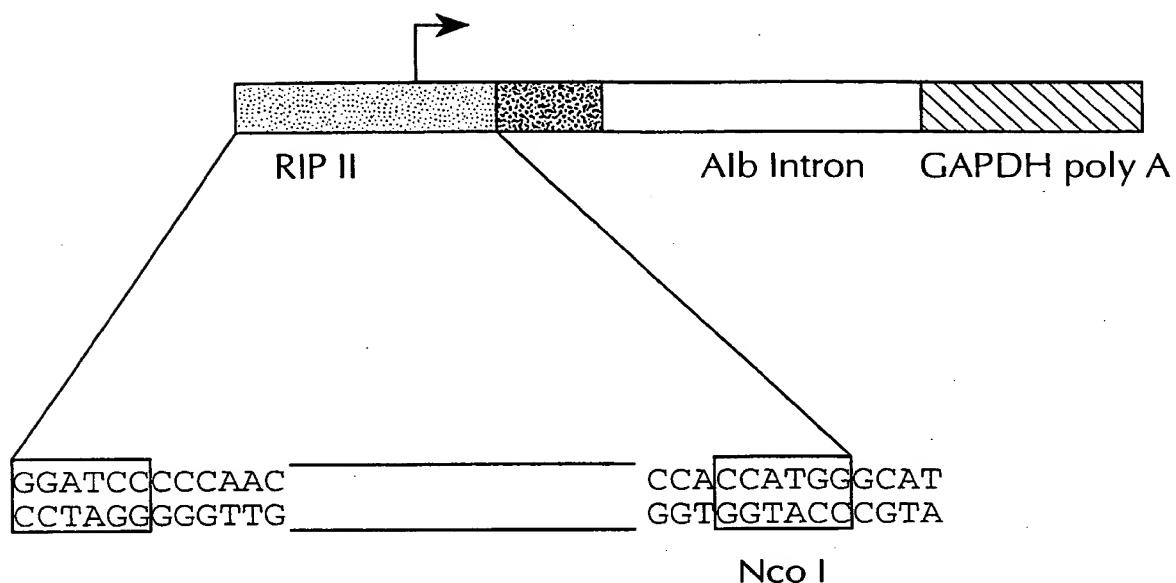
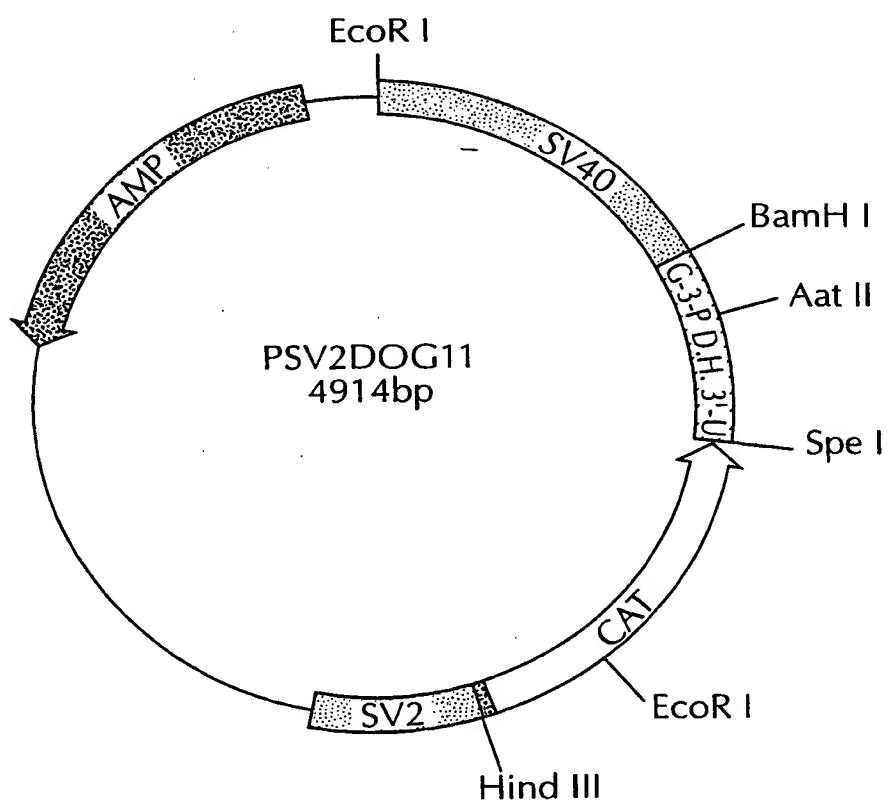
30. A method of evaluating an animal model for a disorder or disease state 5 comprising determining if an IAPP gene in said animal model is expressed at a predetermined level.

31. The method of claim 30 wherein said level is higher than the level in a wild type or normal animal.

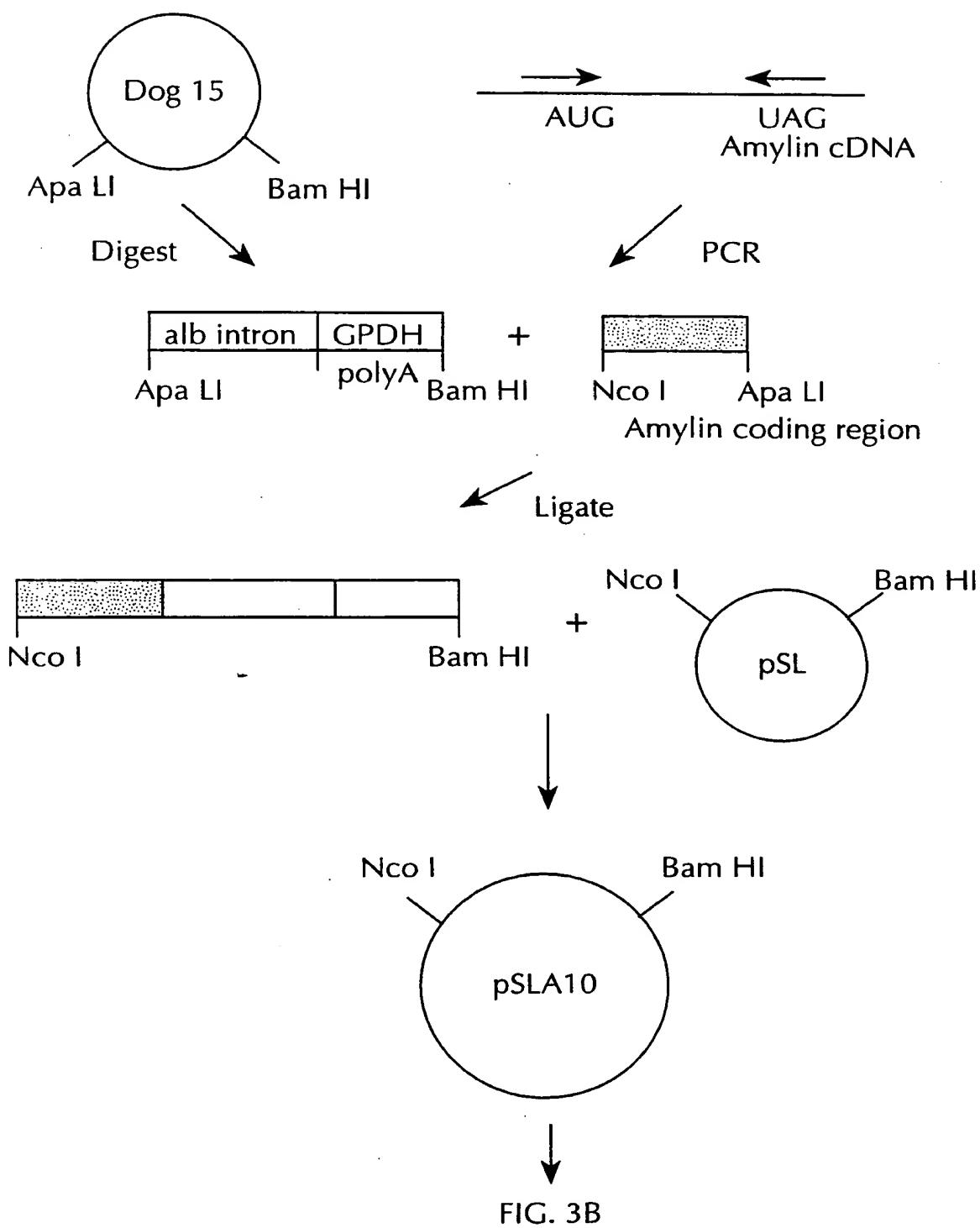
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FIG. 1a**FIG. 1B**

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FIG. 1C**FIG. 2**

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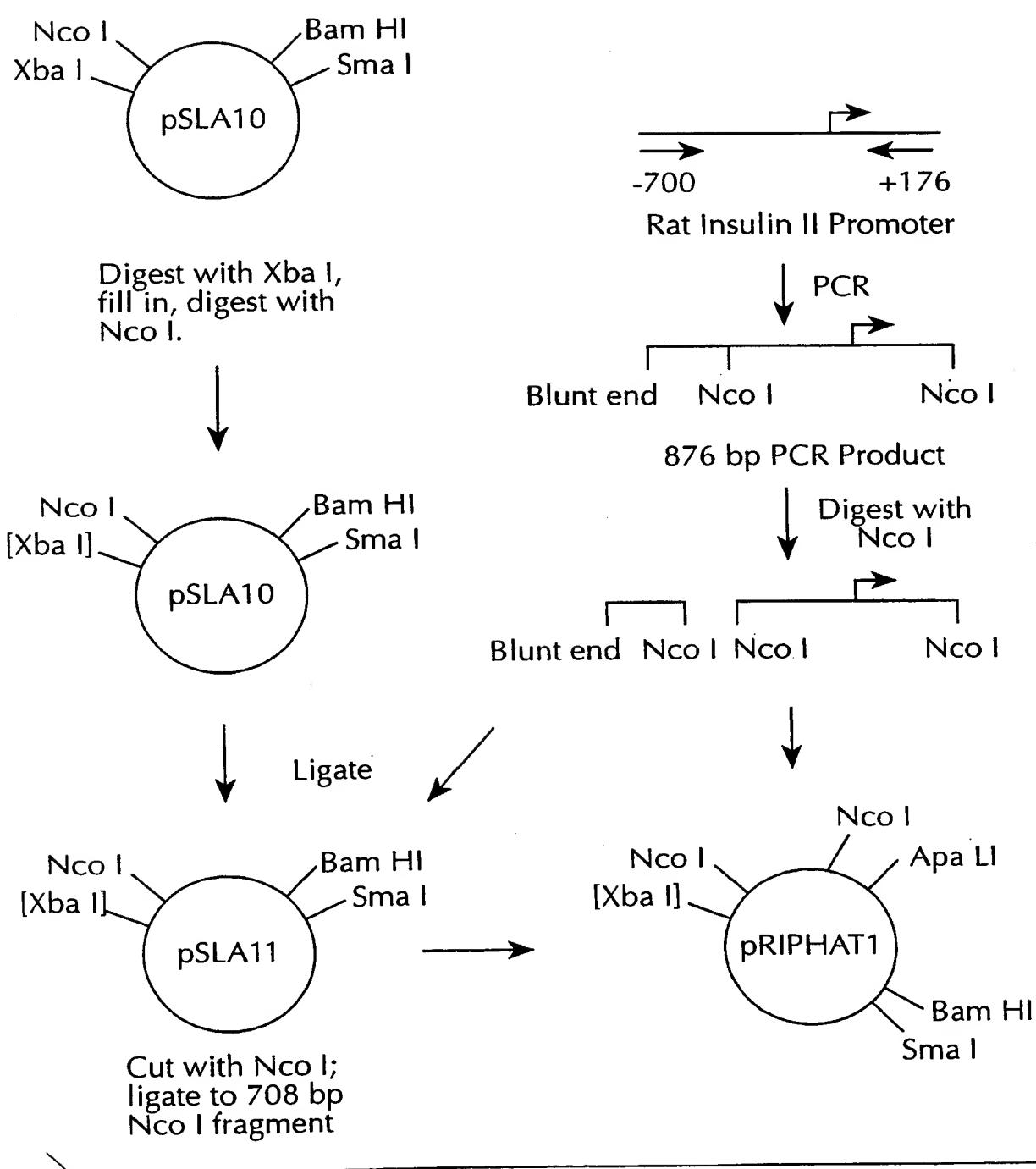
FIG. 3A

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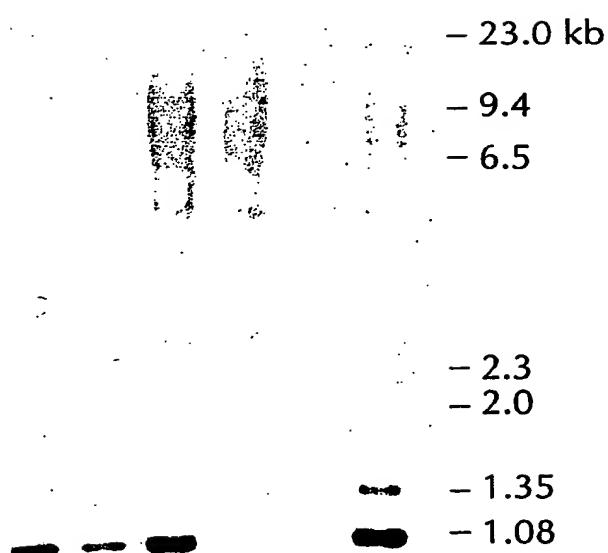
FIG. 3A



FIG. 3B

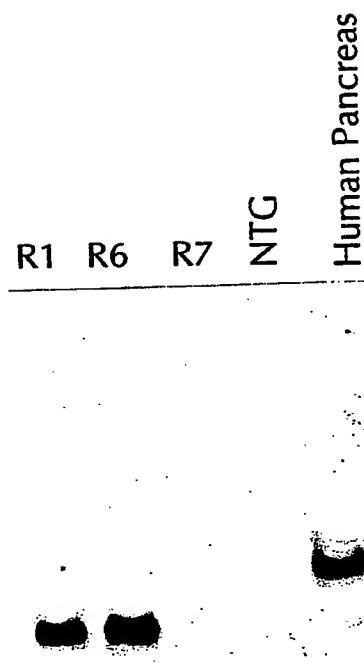


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FIG. 4F1 Progeny: 1 2 3 4 5 6

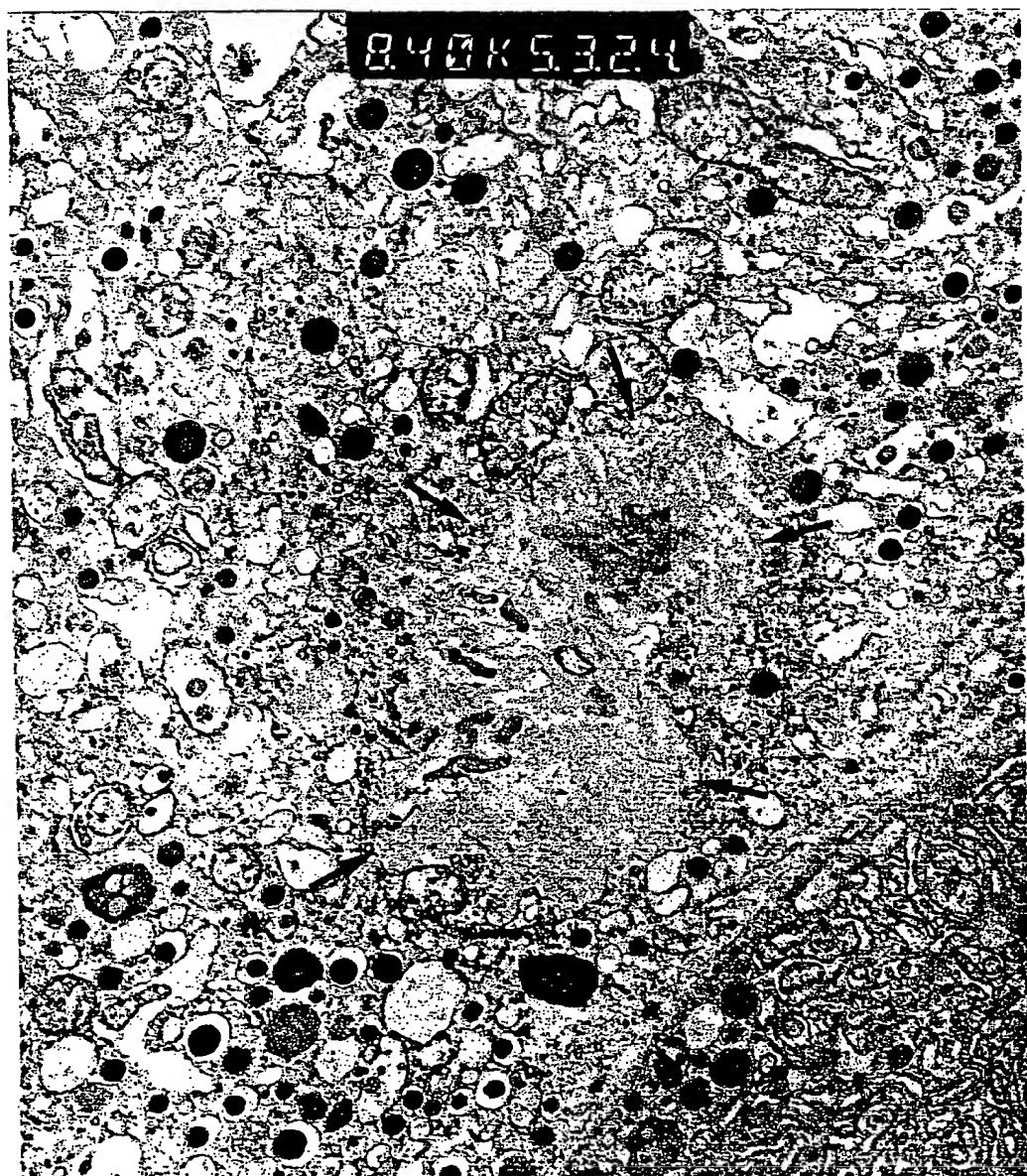
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FIG. 5



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FIG. 6

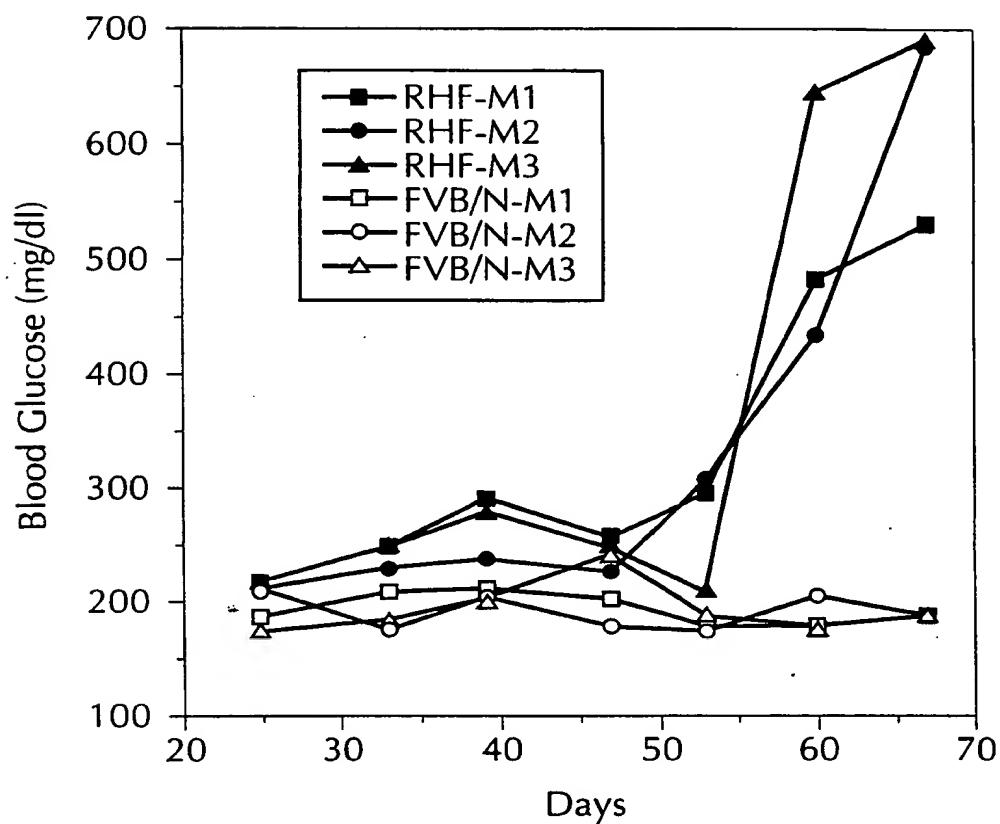


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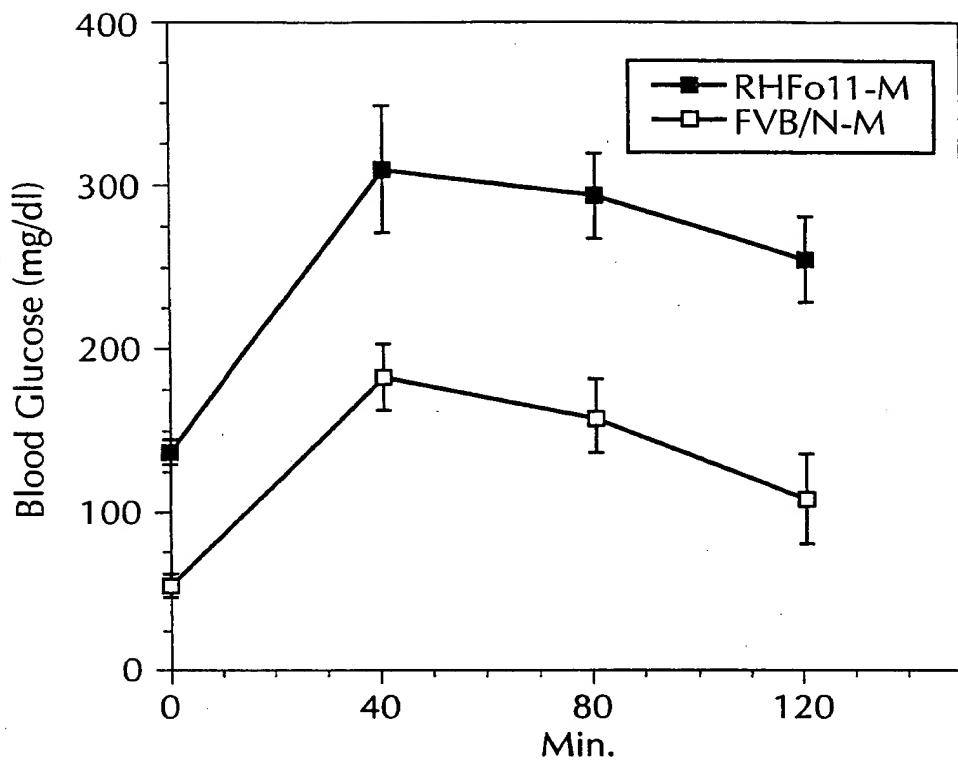
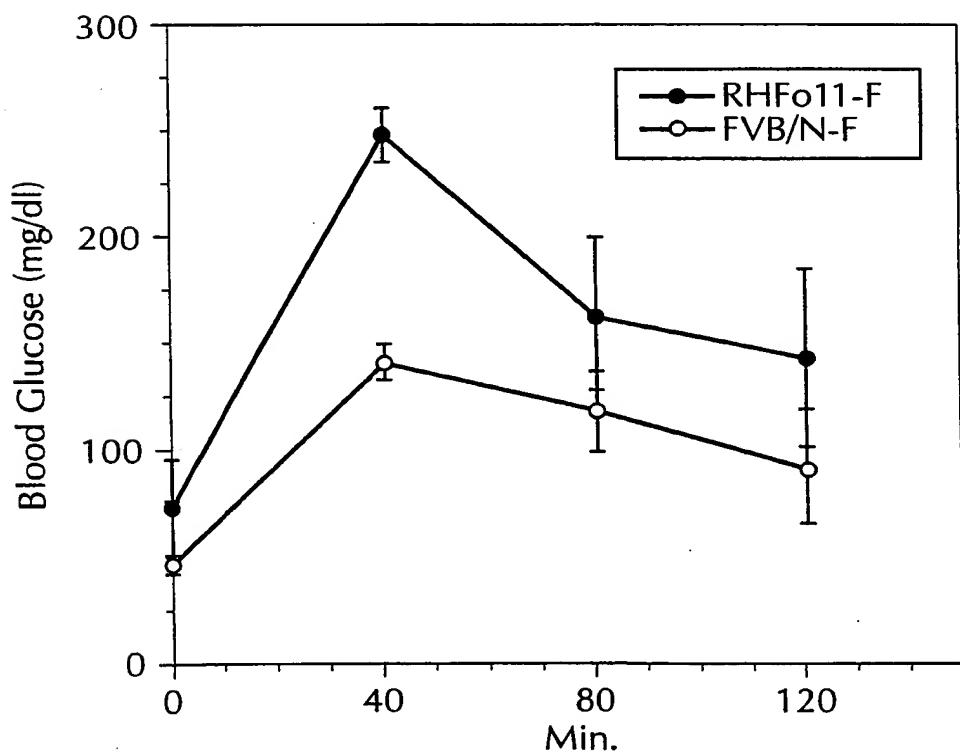
FIG. 7



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FIG. 8

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FIG. 9A**FIG. 9B**

INTERNATIONAL SEARCH REPORT

International Application No
PCT/IB 96/00371

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/16 C12N5/10 A01K67/027 G01N33/50

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 A01K C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	FEBS LETTERS, vol. 323, no. 12, May 1993, pages 40-44, XP002009609 FOX ET AL: "HUMAN ISLET AMYLOID POLYPEPTIDE TRANSGENIC MICE AS A MODEL OF NON-INSULIN-DEPENDENT DIABETES MELLITUS (NIDDM)" cited in the application see the whole document ---	25-31
A	-/-	1-24

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

29 July 1996

Date of mailing of the international search report

09.08.95

Name and mailing address of the ISA

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Fax (+31-70) 340-3016

Authorized officer

Sitch, W

INTERNATIONAL SEARCH REPORT

Int	ional Application No
PCT/IB 96/00371	

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DIABETALOGICA, vol. 36, 1993, pages 1258-1265, XP000576160 HÖPPENER ET AL: "CHRONIC OVERPRODUCTION OF ISLET AMYLOID POLYPEPTIDE/AMYLIN IN TRANSGENIC MICE:LYSOSOMAL LOCALIZATION OF HUMAN ISLET AMYLOID POLYPEPTIDE AND LACK OF MARKED HYPERGLYCAEMIA OR HYPERINSULINAEMIA" cited in the application see page 1258,summary	25-31
A	---	1-24
X	DIABETALOGICA, vol. 37, 1994, pages 725-728, XP000576092 VERCHERE ET AL: "TRANSGENIC MICE OVERPRODUCING ISLET AMYLOID POLYPEPTIDE HAVE INCREASED INSULIN STORAGE AND SECRETION IN VITRO" cited in the application see page 725,summary	25-31
A	---	1-24
X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES,USA, vol. 91, August 1994, pages 8467-8471, XP002009610 DE KONING ET AL: "INTRA-AND EXTRACELLULAR AMYLOID FIBRILS ARE FORMED IN CULTURED PANCREATIC ISLETS OF TRANSGENIC MICE EXPRESSING HUMAN ISLET AMYLOID POLYPEPTIDE" cited in the application see page 8467,abstract	25-31
A	---	1-24
X	EP,A,0 408 294 (AMYLIN CORP) 16 January 1991 see page 4, line 39 - page 5, line 22	25-31
X	EP,A,0 503 827 (PFIZER) 16 September 1992 see claims 1-10	25-31
A	---	1-24
1	JOURNAL OF CELLULAR BIOCHEMISTRY, SUPPLEMENT 0,18 PART A, 1994, XP002009611 SOELLER ET AL: "HUMAN AMYLIN PROMOTER ANALYSIS REVEALS REQUIREMENT FOR BOTH EXON AND INTRON SEQUENCES DOWNSTREAM FROM THE TRANSCRIPTION INITIATION SITE" see abstract C119	

	-/-	

INTERNATIONAL SEARCH REPORT

International Application No
PCT/IB 96/00371

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES, USA, vol. 87, July 1990, pages 5273-5277, XP002009612 NASRIN ET AL: "AN INSULIN RESPONSE ELEMENT IN THE GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE GENE Binds A NUCLEAR PROTEIN INDUCED BY INSULIN IN CULTURED CELLS AND BY NUTRITIONAL MANIPULATIONS IN VIVO" see page 5273, abstract ---	1-24
P,X	AMERICAN JOURNAL OF PATHOLOGY, vol. 147, no. 3, September 1995, pages 609-616, XP000590832 O'BRIEN ET AL: "HUMAN ISLET AMYLOID POLYPEPTIDE EXPRESSION IN COS-1 CELLS. A MODEL OF INTRACELLULAR AMYLOIDogenesis" see page 609, abstract see page 610, paragraph 2 -----	25-31
P,A		1-24

INTERNATIONAL SEARCH REPORT

International application No.

PCT/IB 96/00371

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. **Claims Nos.:**
because they relate to subject matter not required to be searched by this Authority, namely:
Please see Further Information sheet enclosed.
2. **Claims Nos.:**
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. **Claims Nos.:**
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

Remark: Although claims 25, 27-31 and 26 partially insofar as it concerns in vivo method of treatment of (diagnostic method practised on) the human/animal body the search has been carried out and based on the compound/ composition.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IB 96/00371

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
EP-A-0408294	16-01-91	AT-T-	128032	15-10-95
		AU-B-	620727	20-02-92
		AU-B-	5953790	06-02-91
		CA-A-	2020786	11-01-91
		DE-D-	69022501	26-10-95
		DE-T-	69022501	01-02-96
		ES-T-	2080802	16-02-96
		JP-T-	4500688	06-02-92
		US-A-	5364841	15-11-94
		WO-A-	9100737	24-01-91
		US-A-	5280014	18-01-94
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EP-A-0503827	16-09-92	CA-A-	2063005	16-09-92
		JP-A-	5078255	30-03-93
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